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Figure 1. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAgATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 6)

V93E#2

5'-CTTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 7)

V93R#1

5'-gAACATCCCCAAgATAgACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 8)

V93R#2

5'-CTTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 9)

V93N#1

5'-gAACATCCCCAAgATAACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 10)

V93N#2

5'-CTTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 11)

V93H#1

5'-gAACATCCCCAAgATCACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 12)

V93H#2

5'-CTTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 13)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAgATNNKCCCACTATTAgAgAAAAAg-3'

(SEQ ID NO: 14)

V93K#1

5'-gAACATCCCCAAgATAAACCCACTATTAgAg-3' (SEQ ID NO: 43)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 44)

QCM#1 5'-(Phosphate)gAACATCCCCAAgATgCACCCACTATTAgAgAAAAAg-
(SEQ ID NO: 45)'
Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAgATgACCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 46)
Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 47)
Cysteine

QCM#4 5'-
(Phosphate)gAACATCCCCAAgATATACCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 48)
Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAgATATgCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 49)
Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAgATTTCCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 50)
Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 51)
Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 52)
Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACACCCACTATTAgAgAAAAAg- 3'
(SEQ ID NO: 53)
Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3'

(SEQ ID NO: 54)

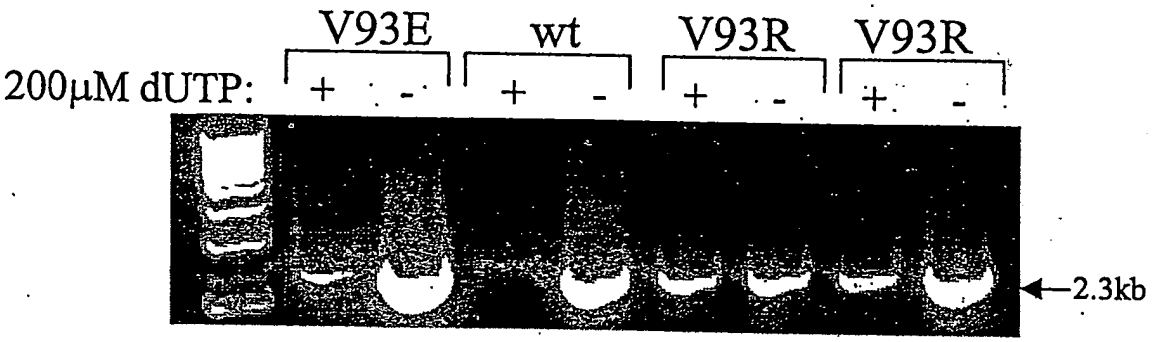
Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCACTATTAgAgAAAAAg-3'

(SEQ ID NO: 55)

Tryptophan

a.)


V93E
wt
V93R
V93R
200μM dUTP:
+ - + - + - + -
2.3kb

b.)

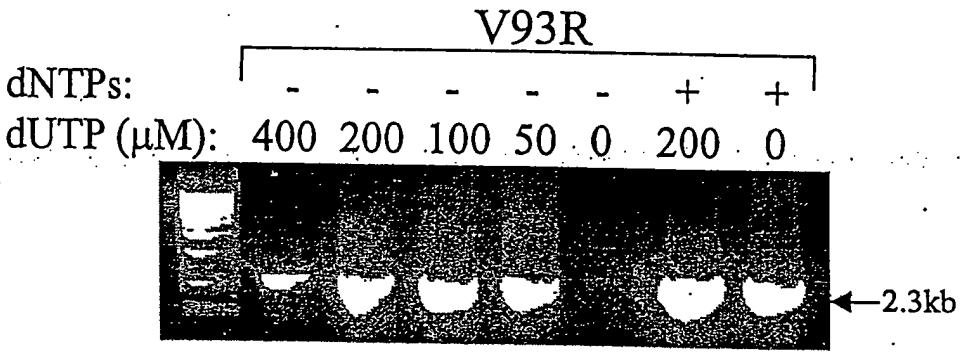

V93R
dNTPs: - - - - - + +
dUTP (μM): 400 200 100 50 0 200 0
2.3kb

Figure 2

Figure 3: Protein concentration, unit concentration, and specific activity of the purified Pfu V93R and V93E mutants.

Pfu mutant	Protein concentration	PCR Unit concentrati	Specific activity (U/mg)
Pfu	0.0258 μg/μl	2.5U/μl	9.7×10^4
Pfu V93R	45 μg/μl	6250U/μl	1.4×10^5
Pfu V93E	35 μg/μl	6250U/μl	1.8×10^5

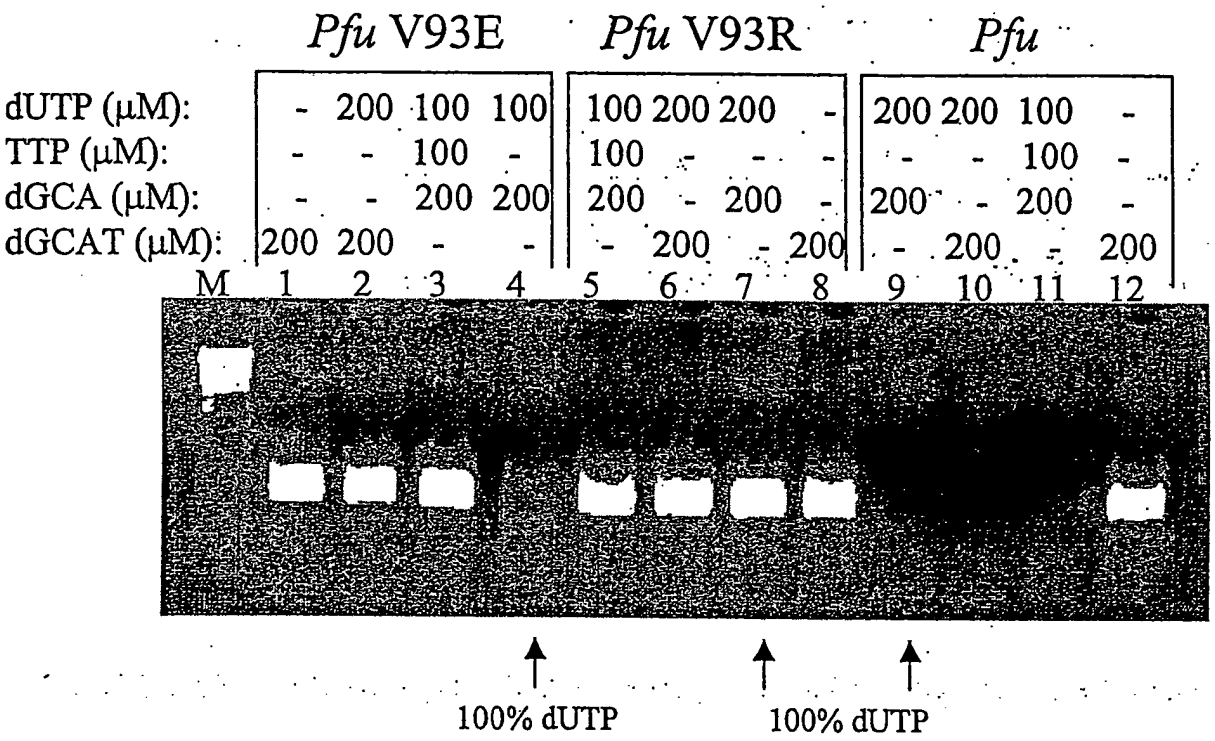

Pfu V93E
Pfu V93R
Pfu
dUTP (μM): - 200 100 100 100 200 200 - 200 200 100 -
TTP (μM): - - 100 - 100 - - - - - 100 -
dGCA (μM): - - 200 200 200 - 200 - 200 - 200 -
dGCAT (μM): 200 200 - - - 200 - 200 - 200 - 200
M 1 2 3 4 5 6 7 8 9 10 11 12
100% dUTP
100% dUTP

Figure 4

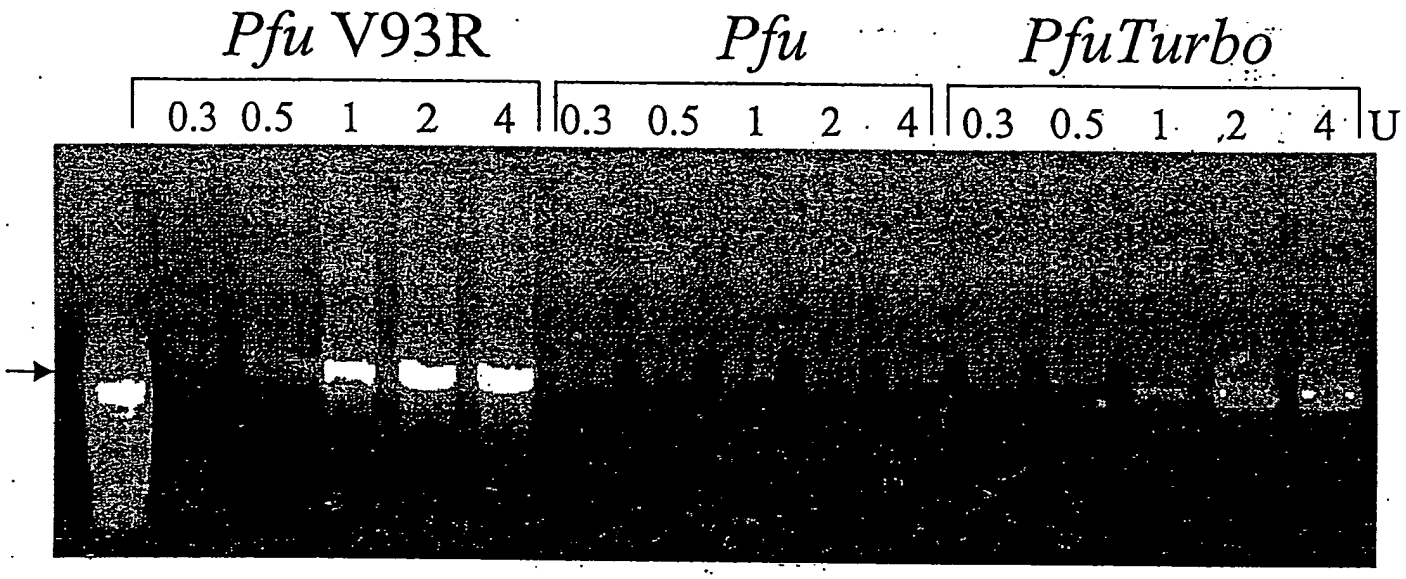


Figure 5

FIGURE 6A

PFU DNA POLYMERASE (SEQ ID NO: 17)
V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATGTTC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

KOD DNA POLYMERASE (SEQ ID NO: 18)
V93R MUTANT: GTC CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTC CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTC CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTC CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTC CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTC CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACGTCC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
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TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
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GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
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GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CTTGA 2325

Vent DNA POLYMERASE (SEQ ID NO: 19)
V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

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CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACGTTC CAGCTATGCG GGGCAAAATA 300
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CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
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GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
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GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
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ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Deep Vent (SEQ ID NO: 20)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACGTTC CCGCAATAAG GGATAAGATA 300
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TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
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GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
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GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
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GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
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TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3 (SEQ ID NO: 21)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTT
CAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCA
AAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGGC
AGGTCTGTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACGTTCCGGCAATCCGCGACAAAATAAGGAAGCA
CCCCGCGGTCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGA
TGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAACC
GGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTCCTTA
CGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGC
TGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACC
CTCGGGAGGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACA
CTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTT
TCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTC
GCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTC
CAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGA
AGGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACgcC
GGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCCTTC
AATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGG
TCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAG
ATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGAT
TCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTA
CGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCA
GACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAA
CTATATCAATCCCAAACTGCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGA
AGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGC
GAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAT
TGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGC
GCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGTGTTAAAATC
CGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGA
GTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCC
TCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGAAG
CCGAAGGGGAAGAAGAAGTGA

Tgo (SEQ ID NO: 22)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATCCTCGATACAGACTACATAACTGAGGATGGAAAGCCCGTCATCAGGATCTTCAAGAAGGAGAACGGCGAGTT
CAAAATAGACTACGACAGAAACTTTGAGCCATACATCTACGCGCTCTTGAAGGACGACTCTGCGATTGAGGACGTCA
AGAAGATAACTGCCGAGAGGCACGGCACTACCGTTAGGGTTGTCAGGGCCGAGAAAGTGAAGAAGAAGTTCCTAGGC
AGGCCGATAGAGGTCTGGAAGCTCTACTTCACTCACCCCCAGGACGTTCCCGCAATCAGGGACAAGATAAAGGAGCA
TCCTGCCGTTGTGGACATCTACGAGTACGACATCCCCTTCGCGAAGCGCTACCTCATAGACAAAGGCTTAATCCCGA
TGGAGGGCGACGAGGAACTTAAGATGCTCGCCTTCGACATCGAGACGCTCTATCACGAGGGCGAGGAGTTCGCCGAA
GGGCCTATCCTGATGATAAGCTACGCCGACGAGGAAGGGGCGCGCGTTATTACCTGGAAGAATATCGACCTTCCCTA
TGTCGACGTCGTTTCCACCGAGAAGGAGATGATAAAGCGCTTCCTCAAGGTCGTCAAGGAAAAGGATCCCGACGTCC
TCATAACCTACAACGGCGACAACTTCGACTTCGCCTACCTCAAGAAGCGCTCCGAGAAGCTCGGAGTCAAGTTCATC
CTCGGAAGGGAAGGGAGCGAGCCGAAAATCCAGCGCATGGGCGATCGCTTTGCGGTGGAGGTCAAGGGAAGGATTCA
CTTCGACCTCTACCCCGTCATTAGGAGAACGATTAACCTCCCCACTTACACCCTTGAGGCAGTATATGAAGCCATCT
TTGGACAGCCGAAGGAGAAGGTCTACGCTGAGGAGATAGCGCAGGCCTGGGAAACGGGCGAGGGATTAGAAAGGGTG
GCCCGCTACTCGATGGAGGACGCAAAGGTAACCTATGAACTCGGAAAAGAGTTCTTCCCTATGGAAGCCCAGCTCTC
GCGCCTCGTAGGCCAGAGCCTCTGGGATGTATCTCGCTCGAGTACCGGAAACCTCGTCGAGTGGTTTTTGCTGAGGA
AGGCCTACGAGAGGAATGAACTTGCACCAAACAAGCCGGACGAGAGGGAGCTGGCAAGAAGAAGGGAGAGCTACGCG
GGTGGATACGTCAAGGAGCCCGAAAGGGGACTGTGGGAGAACATCGTGTATCTGGACTTCCGCTCCCTGTATCCTTC
GATAATAATCACCCATAACGTCTCCCCTGATACACTCAACAGGGAGGGTTGTGAGGAGTACGACGTGGCTCCTCAGG
TAGGCCATAAGTTCTGCAAGGACTTCCCCGGCTTCATCCCAAGCCTCCTCGGAGACCTCTTGGAGGAGAGACAGAAG
GTAAAGAAGAAGATGAAGGCCACTATAGACCCAATCGAGAAGAAACTCCTCGATTACAGGCAACGAGCAATCAAAAT
CCTTGCTAATAGCTTCTACGGTTACTACGGCTATGCAAAGGCCCGCTGGTACTGCAAGGAGTGCGCCGAGAGCGTTA
CCGCTTGGGGCAGGCAGTACATCGAGACCACGATAAGGGAAATAGAGGAGAAATTTGGCTTTAAAGTCCTCTACGCG
GACACAGATGGATTTTTCGCAACAATACCTGGAGCGGACGCCGAAACCGTCAAAAAGAAGGCAAAGGAGTTCCTGGA
CTACATCAACGCCAAACTGCCCGGCCTGCTCGAACTCGAATACGAGGGCTTCTACAAGCGCGGCTTCTTCGTGACGA
AGAAGAAGTACGCGGTTATAGACGAGGAGGACAAGATAACGACGCGCGGGCTTGAAATAGTTAGGCGTGACTGGAGC
GAGATAGCGAAGGAGACGCAGGCGAGGGTTCTTGAGGCGATACTAAAGCACGGTGACGTTGAAGAAGCGGTAAGGAT
TGTCAAAGAGGTTACGGAGAAGCTGAGCAAGTACGAGGTTCCACCGGAGAAGCTGGTCATCTACGAGCAGATAACCC
GCGACCTGAAGGACTACAAGGCCACCGGGCCGCATGTGGCTGTTGCAAAACGCCTCGCCGCAAGGGGGATAAAAATC
CGGCCCGGAACGGTCATAAGCTACATCGTGCTCAAAGGCTCGGGAAGGATTGGGGACAGGGCTATACCCTTTGACGA
ATTTGACCCGGCAAAGCACAAGTACGATGCAGAATACTACATCGAGAACCAGGTTCTTCCAGCTGTGGAGAGGATTC
TGAGGGCCTTTGGTTACCGTAAAGAAGATTTAAGGTATCAGAAAACGCGGCAGGTTGGCTTGGGGGCGTGGCTAAAA
CCTAAGACATGA

PFU DNA POLYMERASE (SEQ ID NO: 23)
G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATGTTC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE (SEQ ID NO: 24)
D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATGTTC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE (SEQ ID NO: 25)
V93 DELETION MUTANT

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT---C CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE (SEQ ID NO: 26)
D92-V93-P94 DELETION MUTANT

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAA ACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480

AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

Figure 6B

>Pfu (SEQ ID NO: 27)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, OR N

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT (SEQ ID NO: 28)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDVPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO (SEQ ID NO: 29)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA

DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD (SEQ ID NO: 30)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDVPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT (SEQ ID NO: 31)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDVPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 (SEQ ID NO: 32)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLG
RSVEVWVLYFTHPQDVPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGT
GPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFT
LGRDGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERV
ARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYA
GGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQK
IKRKMKATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYA
DTDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKGKKK

>Pfu V93/G387P (SEQ ID NO: 33)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, OR N

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93/D141A/E143A (SEQ ID NO: 34)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, OR N

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu delta V93 (SEQ ID NO: 35)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKG
PIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTI
GRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERVA
KYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYT
GGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQK
IKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYI
DTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWS
EIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKI
KPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWLN
IKKS //

>Pfu delta D92-V93-P94 (SEQ ID NO: 36)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPI
IMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGR
DGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERVAKY
SMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGG
FVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIK
TKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDT
DGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEI
AKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKP
GMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWLNIK
KS >Pfu

Figure 6C-1 (SEQ ID NOS: 37[nt] and 38[aa])

5′

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atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc      48
Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
1               5                  10                  15

agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga      96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg
            20                  25                  30

aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att     144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile
        35                  40                  45

gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg     192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg
    50                  55                  60

gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata     240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile
65                  70                  75                  80

gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc     288
Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile
                85                  90                  95

agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac     336
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Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr

100 105 110

gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg 384

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro

115 120 125

atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg 432

Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr

130 135 140

ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata 480

Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile

145 150 155 160

agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc 528

Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile

165 170 175

gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag 576

Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys

180 185 190

cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc 624

Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr

195 200 205

tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag 672

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu
210 215 220

aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa 720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys
225 230 235 240

atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att 768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile
245 250 255

cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act 816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
260 265 270

tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag 864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu
275 280 285

aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga 912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly
290 295 300

tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat 960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305 310 315 320

gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc 1008

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335

gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc 1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca 1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365

cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac 1152
Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr
370 375 380

gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc 1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile
385 390 395 400

gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat 1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
405 410 415

aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac 1296
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Glu Glu Tyr Asp
420 425 430

gtg gct cct cag gta ggc cat aag ttc tgc aag gac ttc ccc ggc ttc 1344

Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
435 440 445

atc cca agc ctc ctc gga gac ctc ttg gag gag aga cag aag gta aag 1392
Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Val Lys
450 455 460

aag aag atg aag gcc act ata gac cca atc gag aag aaa ctc ctc gat 1440
Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys Leu Leu Asp
465 470 475 480

tac agg caa cga gca atc aaa atc ctt gct aat agc ttc tac ggt tac 1488
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr
485 490 495

tac ggc tat gca aag gcc cgc tgg tac tgc aag gag tgc gcc gag agc 1536
Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser
500 505 510

gtt acc gct tgg ggc agg cag tac atc gag acc acg ata agg gaa ata 1584
Val Thr Ala Trp Gly Arg Gln Tyr Ile Glu Thr Thr Ile Arg Glu Ile
515 520 525

gag gag aaa ttt ggc ttt aaa gtc ctc tac gcg gac aca gat gga ttt 1632
Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Phe
530 535 540

ttc gca aca ata cct gga gcg gac gcc gaa acc gtc aaa aag aag gca 1680

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
545 550 555 560

aag gag ttc ctg gac tac atc aac gcc aaa ctg ccc ggc ctg ctc gaa 1728
Lys Glu Phe Leu Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu
565 570 575

ctc gaa tac gag ggc ttc tac aag cgc ggc ttc ttc gtg acg aag aag 1776
Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys
580 585 590

aag tac gcg gtt ata gac gag gag gac aag ata acg acg cgc ggg ctt 1824
Lys Tyr Ala Val Ile Asp Glu Glu Asp Lys Ile Thr Thr Arg Gly Leu
595 600 605

gaa ata gtt agg cgt gac tgg agc gag ata gcg aag gag acg cag gcg 1872
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
610 615 620

agg gtt ctt gag gcg ata cta aag cac ggt gac gtt gaa gaa gcg gta 1920
Arg Val Leu Glu Ala Ile Leu Lys His Gly Asp Val Glu Glu Ala Val
625 630 635 640

agg att gtc aaa gag gtt acg gag aag ctg agc aag tac gag gtt cca 1968
Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
645 650 655

ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac 2016

Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp
660 665 670

tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca 2064
Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
675 680 685

agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc 2112
Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
690 695 700

aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt 2160
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
705 710 715 720

gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag 2208
Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
725 730 735

gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa 2256
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
740 745 750

gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg 2304
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
755 760 765

cta aaa cct aag aca tga 2322

Leu Lys Pro Lys Thr

Tgo93 (R): nnn = AGA, AGG, CGA, CGC, CGG, CGT (R)

Tgo 93 (R) amino acid sequence

Tgo 93 (E): nnn = GAA, GAG (E)

Tgo 93 (E)amino acid sequence

Tgo93 (D): nnn = GAT, GAC (D)

Tgo 93 (D) amino acid sequence

Tgo93 (K): nnn = AAA, AAG (K)

Tgo 93 (K) amino acid sequence

Tgo93 (Q): nnn = CAA, CAG (Q)

Tgo 93 (Q) amino acid sequence

Tgo93 (N): nnn = AAC, AAU (N)

Tgo 93 (N) amino acid sequence

Figure 7A

ACCESSION AAA72101 Vent Thermococcus litoralis

mildtdyitk dgkpiirifk kengefkiel dphfqpyiya llkddsaiee ikaikgerhg ktvrvldavk vrkkflgrev evwklifehp qdvpamrgki rehpavvdiy eydipfakry lidkglipme gdeelkllaf dietfyhegd efgkgeiimi syadeeearv itwknidlpy vdvvsnerem ikrfvqvvke kdpdviityn gdnfdlpyli kraeklgvrl vlgrdkehpe pkiqrmgdsf aveikgrihf dlfpvvrrti nlptytleav yeavlgktks klgaeeiaai weteesmkkl aqysmedara tyelgkeffp meaelaklig qsvwdvsrss tgnlvewyll rvayarnela pnkpdeeeyk rrlrttylgg yvkepekglw eniiyldfrs lypsiivthn vspdtlekeg cknydvapiv gyrfckdfpg fipsilgdli amrqdikkkm kstidpiekk mldyrqraik llansyygym gypkarwysk ecaesvtawg rhyiemtire ieekfgfkvl yadtdgfyat ipgekpelik kkakeflnyi nsklpgllel eyegfylrgf fvtkkryavi deegrittrg levvrrdwse iaketqakvl eailkegsve kavevvrdvv ekiakyrvpl eklviheqit rdlkdykaig phvaiakrla argikvkpgt iisyivlkgs gkisdrvill teydprkhky dpdyyienqv lpavlrilea fgyrkedlry qsskqtglda wlkr (SEQ ID NO. 83)

ACCESSION O33845 THEST THERMOCOCCUS SP.

mildtdyitk dgkpiirifk kengefkiel dphfqpyiya llkddsaide ikaikgerhg kivrvvdavk vkkkflgrdv evwklifehp qdvpalrgki rehpavidiy eydipfakry lidkglipme gdeelklmaf dietfyhegd efgkgeiimi syadeeearv itwknidlpy vdvvsnerem ikrfvqivre kdpdvlityn gdnfdlpyli kraeklgvtl llgrdkehpe pkihrmgdsf aveikgrihf dlfpvvrrti nlptytleav yeavlgktks klgaeeiaai weteesmkkl aqysmedara tyelgkeffp meaelaklig qsvwdvsrss tgnlvewyll rvayernela pnkpdeeeyr rrlrttylgg yvkeperglw eniayldfrc hpadtkvivk gkgivnisdv kegdyilgid gwqrvkkvwk yhyegklini nglkctpnhk vpvvtendrq trirdslaks flsgkvkgki ittklfekia efeknkpsee eilkgelsgi ilaegtllrk dieyfdssrg kkrishqyrv eitigeneke llerilyifd klfgirpsvk kkgdtnalki ttakkavylq ieellknies lyapavlrgf ferdatvnki rstivvtqgt nnkwkidiva klldslgipy sryeykyien gkeltkhile itgrdglilf qtlvgfisse knealekaie vremnrlknn sfynlstfev sseyykgevy dltlegnpyy fangilthns lypsiivthn vspdtlereg cknydvapiv gykfckdfpg fipsilgeli tmrqeikkkm katidpiekk mldyrqravk llansilpne wlpiiengev kfvkigefid rymeeqkdkv rtvdntevle vdnifafsln keskkseikk vkalirhkyk geayevelns grkihitrgh slftirngki keiwgeevkv gdliivpkkv klnekeavin ipelisklpd edtadvvmtt pvkgrknffk gmlrtlkwif geeskrirtf nrylfhleel gfvkllprgy evtdweglkr yrqlyeklvk nlryngnkre ylvrfndikd svscfprkel eewkigtxkg frxkcilkvd edfgkflgyy vsegyagaqk nktggmsysv klynenpnvl kdmkniaekf fgkvrvgknc vdipkkmayl lakslcgvta enkripsiif dssepvrwaf lrayfvgdgd ihpskrlrls tksellanql vfllnslgvs sikigfdsgv yrvyinedlp flqtsrqknt yypnlipkev leeifgrkfq knitfekfke ladsgkldkr kvklldflln gdivldrvkn vekreyegyv ydlsvednen flvgfgllya hnsyygymgy pkarwyskec aesvtawgrh yiemtikeie ekfgfkvlya dsvtgdteii vkrngriefv pieklfervd yrigekeyci ledvealtld nrgkliwkkv pyvmrhrakk kvyriwitns wyidvtedhs livaedglke arpmeiegks liatkddlsg veyikphaie eisyngyvyd ievegthrff angilvhntd gfyatipgek petikkkake flkyinsklp glleleyegf ylrgffvakk ryavideegr ittrglevvr rdwseiaket qakvleailk edsvekavei vkdvveeiak yqvpleklvi heqitkdlse ykaigphvai akrlaakgik vrpgtiisyi vlrgsgkisd rvillseydp kkhkydpdyy ienqvlpavl rileafgyrk edlkyqsskq vgldawlkk (SEQ ID NO. 84)

ACCESSION P77916 Pab Pyrococcus abyssi

miidadyite dgkpiirifk kekgefkvey drtfrpyiya llkddsaide vkkitaerhg kivritevek vqkkflgrpi evwklylehp qdvpaireki rehpavvdif eydipfakry lidkgltpme gneeltflav dietlyhege efgkgpiimi syadeegakv itwksidlpy vevvsserem ikrlvkvire kdpdviityn gdnfdfpyll kraeklgikl plgrdnsepk mqrmgdslav eikgrihfdl fpvirrtinl ptytleavye aifgkskekv yaheiaeawe tgkglervak ysmedakvtf elgkeffpme aqlarlvgqp vwdvsrsstg nlvewfllrk ayernelapn kpdereyerr lresyeggyv kepekglweg ivsldfrsly psiiithnvs pdtlnrenck eydvapqvgh rfckdfpgfi psllgnllee rqkikkrmke skdpvekkll dyrqraikil ansyygyygy akarwyckec aesvtawgrq yidlvrrele srgfkvlyid tdglyatipg akheeikeka lkfveyinsk lpglleleye gfyargffvt kkkyalidee gkivtrglei vrrdwseiak etqakvleai lkhgnvdeav kivkevtekl skyeippekl viyeqitrpl seykaigphv avakrlaakg vkvkpgmvig yivlrgdgpi skraiaieef dpkkhkydae yyienqvlpa verilrafgy rkedlkyqkt kqvglgawlk f (SEQ ID NO. 85)

ACCESSION O59610 PYRHO Pyrococcus horikoshii

mildadyite dgkpiirifk kengefkvey drnfrpyiya llrddsaide ikkitaqrhg kvvrivetek iqrkflgrpi evwklylehp qdvpairdki rehpavvdif eydipfakry lidkgltpme gnekltflav dietlyhege efgkgpvimi syadeegakv itwkkidlpy vevvsserem ikrlirvike kdpdviityn gdnfdfpyll kraeklgikl llgrdnsepk mqkmgdslav eikgrihfdl fpvirrtinl ptytleavye aifgkpkekv yadeiakawe tgeglervak ysmedakvty elgreffpme aqlarlvgqp vwdvsrsstg nlvewfllrk ayernelapn kpdekeyerr lresyeggyv kepekglweg ivsldfrsly psiiithnvs pdtlnregce eydvapkvgh rfckdfpgfi psllgqllee rqkikkrmke skdpvekkll dyrqraikil ansilpdewl pivenekvrf vkigdfidre ieenaervkr dgeteilevk dlkalsfnre tkkselkkvk alirhrysgk vysiklksgr rikitsghsl fsvkngklvk vrgdelkpgd lvvvpgrlkl peskqvlnlv elllklpeee tsnivmmipv kgrknffkgm lktlywifge gerprtagry lkhlerlgyv klkrrgcevl dweslkryrk lyetliknlk yngnsraymv efnslrdvvs lmpieelkew iigeprgpki gtfidvddsf akllgyyiss gdvekdrvkf hskdqnvled iaklaeklfg kvrrgrgyie vsgkishaif rvlaegkrip efiftspmdi kvaflkglng naeeltfstk sellvnqlil llnsigvsdi kiehekgvyr vyinkkessn gdivldsves ievekyegyv ydlsvednen flvgfgllya hnsyygyygy akarwyckec aesvtawgrq yidlvrrele argfkvlyid tdglyatipg vkdweevkrr alefvdyins klpgvleley egfyargffv tkkkyalide egkivtrgle ivrrdwseia ketqarvlea ilkhgnveea vkivkdvtek ltnyevppek lviyeqitrp ineykaigph vavakrlmar gikvkpgmvi gyivlrgdgp iskraisiee fdprkhkyda eyyienqvlp averilkafg ykredlrwqk tkqvglgawi kvkks (SEQ ID NO. 86)

ACCESSION P77932 PYRSE PYROCOCCUS SP.

miidadyite dgkpiirifk kekgefkvey drtfrpyiya llkddsaide vkkitaerhg kivritevek vqkkflgrpi evwklylehp qdvpaireki rehpavvdif eydipfakry lidkgltpme gneeltflav dietlyhege efgkgpiimi syadeegakv itwksidlpy vevvsserem ikrlvkvire kdpdviityn gdnfdfpyll kraeklgikl plgrdnsepk mqrmgdslav eikgrihfdl fpvirrtinl ptytleavye aifgkskekv yaheiaeawe tgkglervak ysmedakvtf elgkeffpme aqlarlvgqp vwdvsrsstg nlvewfllrk ayernelapn kpdereyerr lresyeggyv kepekglweg ivsldfrsly psiiithnvs pdtlnrenck eydvapqvgh rfckdfpgfi psllgnllee rqkikkrmke skdpvekkll dyrqraikil ansyygyygy akarwyckec aesvtawgrq yidlvrrele ssgfkvlyid tdglyatipg akpneikeka lkfveyinsk lpglleleye gfyargffvt kkkyalidee gkivtrglei vrrdwseiak etqakvleai lkhgnvdeav kivkevtekl skyeippekl viyeqitrpl seykaigphv avakrlaakg vkvkpgmvig yivlrgdgpi skraiaieef dpkkhkydae yyienqvlpa verilrafgy rkedlryqkt kqvglgawlk f (SEQ ID NO. 87)

ACCESSION AAA67131 DeepVent Pyrococcus sp.

mildadyite dgkpiirifk kengefkvey drnfrpyiya llkddsqide vrkitaerhg kivriidaek vrkkflgrpi evwrlyfehp qdvpairdki rehsavidif eydipfakry lidkglipme gdeelkllaf dietlyhege efakgpiimi syadeeeakv itwkkidlpy vevvsserem ikrflkvire kdpdviityn gdsfdlpylv kraeklgikl plgrdgsepk mqrlgdmtav eikgrihfdl yhvirrtinl ptytleavye aifgkpkekv yaheiaeawe tgkglervak ysmedakvty elgreffpme aqlsrlvgqp lwdvsrsstg nlvewyllrk ayernelapn kpdereyerr lresyaggyv kepekglweg lvsldfrsly psiiithnvs pdtlnregcr eydvapevgh kfckdfpgfi psllkrllde rqeikrkmka skdpiekkml dyrqraikil ansyygyygy akarwyckec aesvtawgre yiefvrkele ekfgfkvlyi dtdglyatip gakpeeikkk alefvdyina klpglleley egfyvrgffv tkkkyalide egkiitrgle ivrrdwseia ketqakvlea ilkhgnveea vkivkevtek lskyeippek lviyeqitrp lheykaigph vavakrlaar gvkvrpgmvi gyivlrgdgp iskrailaee fdlrkhkyda eyyienqvlp avlrileafg yrkedlrwqk tkqtgltawl nikkk (SEQ ID NO. 88)

ACCESSION P80061 Pfu Pyrococcus furiosus

mildvdyite egkpvirlfk kengkfkieh drtfrpyiya llrddskiee vkkitgerhg kivrivdvek vekkflgkpi tvwklylehp qdvptirekv rehpavvdif eydipfakry lidkglipme geeelkilaf dietlyhege efgkgpiimi syadeneakv itwknidlpy vevvsserem ikrflriire kdpdiivtyn gdsfdfpyla kraeklgikl tigrdgsepk mqrigdmtav evkgrihfdl yhvitrtinl ptytleavye aifgkpkekv yadeiakawe sgenlervak ysmedakaty elgkeflpme iqlsrlvgqp lwdvsrsstg nlvewfllrk ayernevapn kpseeeyqrr lresytggfv kepekglwen ivyldfraly psiiithnvs pdtlnlegck nydiapqvgh kfckdipgfi psllghllee rqkiktkmke tqdpiekill dyrqkaikll ansfygyygy akarwyckec aesvtawgrk yielvwkele ekfgfkvlyi dtdglyatip ggeseeikkk alefvkyins klpglleley egfykrgffv tkkryavide egkvitrgle ivrrdwseia ketqarvlet ilkhgdveea vrivkeviqk lanyeippek laiyeqitrp lheykaigph vavakklaak gvkikpgmvi gyivlrgdgp isnrailaee ydpkkhkyda eyyienqvlp avlrilegfg yrkedlryqk trqvgltswl nikks (SEQ ID NO. 89)

> JDF-3 Thermococcus sp.

mildvdyitengkpvirvfkkengefrieydrefepyfyallrddsaieeikkitaerhgrvvkvkraekvkkkflgrsvevwvlyfthp qdvpairdkirkhpavidiyeydipfakrylidkglipmegeeelklmsfdietlyhegeefgtgpilmisyadesearvitwkkidlpy vevvstekemikrflrvvkekdpdvlityngdnfdfaylkkrceklgvsftlgrdgsepkiqrmgdrfavevkgrvhfdlypvirrtinl ptytleavyeavfgkpkekvyaeeiatawetgeglervarysmedarvtyelgreffpmeaqlsrligqglwdvsrsstgnlvewfllrk ayernelapnkpderelarrrggyaggyvkeperglwdnivyldfrslypsiiithnvspdtlnregcrsydvapevghkfckdfpgfip sllgnlleerqkikrkmkatldpleknlldyrqraikilansyygyygyararwycrecaesvtawgreyiemvireleekfgfkvlyadt dglhatipgadaetvkkkameflnyinpklpglleleyegfyvrgffvtkkkyavideegkittrgleivrrdwseiaketqarvleailrh gdveeavrivrevteklskyevppeklviheqitrelkdykatgphvaiakrlaargvkirpgtvisyivlkgsgrigdraipfdefdptkh kydadyyienqvlpaverilrafgyrkedlryqktrqvglgawlkpkgkkk(SEQ ID NO. 90)

ACCESSION Q56366 9degN THERMOCOCCUS SP. (STRAIN 9°N-7).

mildtdyite ngkpvirvfk kengefkiey drtfepyfya llkddsaied vkkvtakrhg tvvkvkraek vqkkflgrpi evwklyfnhp qdvpairdri rahpavvdiy eydipfakry lidkglipme gdeeltmlaf dietlyhege efgtgpilmi syadgsearv itwkkidlpy vdvvstekem ikrflrvvre kdpdvlityn gdnfdfaylk krceelgikf tlgrdgsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye avfgkpkekv yaeeiaqawe sgeglervar ysmedakvty elgreffpme aqlsrligqs lwdvsrsstg nlvewfllrk aykrnelapn kpderelarr rggyaggyvk eperglwdni vyldfrslyp siiithnvsp dtlnregcke ydvapevghk fckdfpgfip sllgdlleer qkikrkmkat vdplekklld yrqraikila nsfygyygya karwyckeca esvtawgrey iemvirelee kfgfkvlyad tdglhatipg adaetvkkka keflkyinpk lpglleleye gfyvrgffvt kkkyavidee gkittrglei vrrdwseiak etqarvleai lkhgdveeav rivkevtekl skyevppekl viheqitrdl rdykatgphv avakrlaarg vkirpgtvis yivlkgsgri gdraipadef dptkhrydae yyienqvlpa verilkafgy rkedlryqkt kqvglgawlk vkgkk (SEQ ID NO. 91)

ACCESSION BAA06142 KOD Pyrococcus sp.

mildtdyite dgkpvirifk kengefkiey drtfepyfya llkddsaiee vkkitaerhg tvvtvkrvek vqkkflgrpv evwklyfthp qdvpairdki rehpavidiy eydipfakry lidkglvpme gdeelkmlaf dietlyhege efaegpilmi syadeegarv itwknvdlpy vdvvsterem ikrflrvvke kdpdvlityn gdnfdfaylk krceklginf algrdgsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye avfgqpkekv yaeeittawe tgenlervar ysmedakvty elgkeflpme aqlsrligqs lwdvsrsstg nlvewfllrk ayernelapn kpdekelarr rqsyeggyvk eperglweni vyldfrchpa dtkvvvkgkg iinisevqeg dyvlgidgwq rvrkvweydy kgelvningl kctpnhklpv vtknerqtri rdslaksflt kkvkgkiitt plfyeigrat senipeeevl kgelagilla egtllrkdve yfdssrkkrr ishqyrveit igkdeeefrd rityiferlf gitpsisekk gtnavtlkva kknvylkvke imdnieslha psvlrgffeg dgsvnrvrrs ivatqgtkne wkiklvskll sqlgiphqty tyqyqengkd rsryileitg kdglilfqtl igfiserkna llnkaisqre mnnlenngfy rlsefnvste yyegkvydlt legtpyyfan gilthnslyp siiithnvsp dtlnregcke ydvapqvghr fckdfpgfip sllgdlleer qkikkkmkat idpierklld yrqraikila nsilpeewlp vleegevhfv rigelidrmm eenagkvkre getevlevsg levpsfnrrt nkaelkrvka lirhdysgkv ytirlksgrr ikitsghslf svrngelvev tgdelkpgdl vavprrlelp ernhvlnlve lllgtpeeet ldivmtipvk gkknffkgml rtlrwifgee krprtarryl rhledlgyvr lkkigyevld wdslknyrrl yealvenvry ngnkreylve fnsirdavgi mplkelkewk igtlngfrmr klievdesla kllgyyvseg yarkqrnpkn gwsysvklyn edpevlddme rlasrffgkv rrgrnyveip kkigyllfen mcgvlaenkr ipefvftspk gvrlaflegy figdgdvhpn krlrlstkse llanqlvlll nsvgvsavkl ghdsgvyrvy ineelpfvkl dkkknayysh vipkevlsev fgkvfqknvs pqtfrkmved grldpekaqr lswliegdvv ldrvesvdve dydgyvydls vednenflvg fglvyahnsy ygyygyarar wyckecaesv tawgreyitm tikeieekyg fkviysdtdg ffatipgada etvkkkamef lkyinaklpg aleleyegfy krgffvtkkk yavideegki ttrgleivrr dwseiaketq arvleallkd gdvekavriv kevteklsky evppeklvih eqitrdlkdy katgphvava krlaargvki rpgtvisyiv lkgsgrigdr aipfdefdpt khkydaeyyi enqvlpaver ilrafgyrke dlryqktrqv glsawlkpkg t (SEQ ID NO. 92)

ACCESSION 4699806 Tgo Thermococcus gorgonarius.

mildtdyite dgkpvirifk kengefkidy drnfepyiya llkddsaied vkkitaerhg ttvrvvraek vkkkflgrpi evwklyfthp qdvpairdki kehpavvdiy eydipfakry lidkglipme gdeelkmlaf dietlyhege efaegpilmi syadeegarv itwknidlpy vdvvstekem ikrflkvvke kdpdvlityn gdnfdfaylk krseklgvkf ilgregsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye aifgqpkekv yaeeiaqawe tgeglervar ysmedakvty elgkeffpme aqlsrlvgqs lwdvsrsstg nlvewfllrk ayernelapn kpderelarr resyaggyvk eperglweni vyldfrslyp siiithnvsp dtlnregcee ydvapqvghk fckdfpgfip sllgdlleer qkvkkkmkat idpiekklld

yrqraikila nsfygyygya karwyckeca esvtawgrqy iettireiee kfgfkvlyad tdgffatipg adaetvkkka kefldyinak lpglleleye gfykrgffvt kkkyavidee dkittrglei vrrdwseiak etqarvleai lkhgdveeav rivkevtekl skyevppekl viyeqitrdl kdykatgphv avakrlaarg ikirpgtvis yivlkgsgri gdraipfdef dpakhkydae yyienqvlpa verilrafgy rkedlryqkt rqvglgawlk pkt (SEQ ID NO. 93)

ACCESSION P74918 THEFM Thermococcus fumicolans

mildtdyite dgrpvirvfk kengefkiey drdfepyiya llkddsaied vkkitasrhg ttvrvvragk vkkkflgrpi evwklyfthp qdvpairdki rehpavvdiy eydipfakry lidkglipme gdeelkmlaf dietlyhege efaegpilmi syadeegarv itwkkidlpy vdvvstekem ikrflkvvke kdpdvlityn gdnfdfaylk krseklgvkf ilgrdgsepk iqrmgdrfav evkgrihfdl ypvirhtinl ptytleavye aifgqpkekv yaeeiaqawe tgeglervar ysmedakvty elgreffpme aqlsrlvgqs fwdvsrsstg nlvewyllrk ayernelapn kpsgrelerr rggyaggyvk eperglweni ayldfrchpa dtkvivkgkg vvnisevreg dyvlgidgwq kvqrvweydy egelvningl kctpnhklpv vrrterqtai rdslaksflt kkvkgklitt plfekigkie redvpeeeil kgelagiila egtllrkdve yfdssrgkkr vshqyrveit vgaqeedfqr rivyiferlf gvtpsvyrkk ntnaitfkva kkevylrvre imdgienlha psvlrgffeg dgsvnkvrkt vvvnqgtnne wkievvskll nklgiphrry tydyterekt mtthileiag rdglilfqti vgfisteknm aleeairnre vnrlennafy tladftakte yykgkvydlt legtpyyfan gilthnslyp siiishnvsp dtlnregcge ydeapqvghr fckdfpgfip sllgdllder qkvkkhmkat vdpiekklld yrqraikila nsfygyygya karwyckeca esvtawgrqy iettmreiee kfgfkvlyad svtgdtevti rrngriefvp ieklfervdh rvgekeycvl ggvealtldn rgrlvwkkvp yvmrhktdkr iyrvwftnsw yldvtedhsl igylntskvk pgkplkerlv evkpeelggk vkslitpnrp iartikanpi avklweligl lvgdgnwggq snwakyyvgl scgldkaeie rkvlnplrea svisnyydks kkgdvsilsk wlagfmvkyf kdengnkaip sfmfnlprey ieaflrglfs adgtvslrrg ipeirltsvn relsdavrkl lwlvgvsnsl ftetkpnryl ekesgthsih vriknkhrfa drigflidrk stklsenlgg htnkkrayky dfdlvyprki eeitydgyvy dievegthrf fangilvhnt dgffatipga daetvkkkar eflnyinpkl pglleleyeg fyrrgffvtk kkyavideeg kittrgleiv rrdwsevake tqarvleail rhgdveeavr ivkevtekls kyevppeklv iheqitrelk dykatgphva iakrlaargi kvrpgtvisy ivlkgsgrig drtipfdefd ptkhrydaey yienqvlpav erilkafgyk kedlryqktr qvglgawlkm gkk (SEQ ID NO. 94)

ACCESSION O27276 METTH Methanobacterium thermoautotrophicum

medyrmvlld idyvtvdevp virlfgkdks ggnepiiahd rsfrpyiyai ptdldeclre leelelekle vkemrdlgrp teviriefrh pqdvpkirdr irdlesvrdi rehdipfyrr ylidksivpm eelefqgvev dsapsvttdv rtvevtgrvq stgsgahgld ilsfdievrn phgmpdpekd eivmigvagn mgyesvista gdhldfvevv ederellerf aeividkkpd ilvgynsdnf dfpyitrraa ilgaeldlgw dgskirtmrr gfanataikg tvhvdlypvm rrymnldryt lervyqelfg eekidlpgdr lweywdrdel rdelfrysld dvvathriae kilplnlelt rlvgqplfdi srmatgqqae wflvrkayqy gelvpnkpsq sdfssrrgrr avggyvkepe kglhenivqf dfrslypsii isknispdtl tddeesecyv apeygyrfrk sprgfvpsvi geilservri keemkgsddp merkilnvqq ealkrlantm ygvygysrfr wysmecaeai tawgrdyikk tiktaeefgf htvyadtdgf yatyrg (SEQ ID NO. 95)

ACCESSION Q58295 Metja Methanococcus jannaschii

mgmsmgkiki dalidntykt iedkaviyly linsilkdrd fkpyfyvelh kekvenedie kikefllknd llkfveniev vkkiilrkek evikiiathp qkvpklrkik eceivkeiye hdipfakryl idneiipmty wdfenkkpvs ieipklksva fdmevynrdt epnperdpil masfwdengg kvitykefnh pnievvknek elikkiietl keydviytyn gdnfdfpylk arakiygidi nlgkdgeelk ikrggmeyrs yipgrvhidl ypisrrllkl tkytledvvy nlfgieklki phtkivdywa nndktlieys lqdakytyki gkyffplevm fsrivnqtpf eitrmssgqm veyllmkraf kenmivpnkp deeeyrrrvl ttyeggyvke pekgmfedii smdfrchpkg tkvvvkgkgi vniedvkegn yvlgidgwqk vkkvwkyeye gelinvnglk ctpnhkiplr ykikhkkink ndylvrdiya kslltkfkge gklilckdfe tignyekyin dmdedfilks eligillaeg hllrrdieyf dssrgkkris hqyrveitvn edekdfieki kyifkklfny elyvrrkkgt kaitlgcakk diylkieeil knkekylpna ilrgffegdg yvntvrravv vnqgtnnydk ikfiaslldr lgikysfyty syeergkklk ryvieifskg dlikfsilis fisrrknnll neiirqktly kigdygfydl ddvcvslesy kgevydltle grpyyfangi lthnslypsi iisynispdt ldcecckdvs ekilghwfck kkeglipktl rnlierrini krrmkkmaei geineeynll dyeqkslkil ansilpdeyl tiieedgikv vkigeyiddl mrkhkdkikf sgiseiletk nlktfsfdki tkkceikkvk alirhpyfgk aykiklrsgr tikvtrghsl fkyengkive vkgddvrfgd livvpkkltc vdkevvinip krlinadeee ikdlvitkhk dkaffvklkk tlediennkl kvifddcily lkelglidyn iikkinkvdi kildeekfka ykkyfdtvie hgnfkkgrcn iqyikikdyi anipdkefed ceigaysgki nallkldekl akflgffvtr grlkkqklkg etvyeisvyk slpeyqkeia etfkevfgag smvkdkvtmd nkivylvlky ifkcgdkdkk hipeelflas esviksfldg flkakknshk gtstfmakde kylnqlmilf nlvgiptrft pvknkgyklt lnpkygtvkd lmldevkeie afeysgyvyd lsvednenfl vnniyahnsv ygylafprar fysrecaeiv tylgrkyile tvkeaekfgf kvlyidtdgf yaiwkekisk eelikkamef veyinsklpg tmelefegyf krgifvtkkr yalidengrv tvkglefvrr dwsniakitq rrvleallve gsiekakkii qdvikdlrek kikkedliiy tqltkdpkey kttaphveia kklmregkri kvgdiigyii vkgtksiser aklpeevdid didvnyyidn qilppvlrim eavgvsknel kkegaqltld kffk (SEQ ID NO. 96)

ACCESSION B56277 POC Pyrodictium occultum

mtetiefvll dssyeilgke pvvilwgitl dgkrvvlldh rfrpyfyali argyedmvee iaasirrlsv vkspiidakp ldkryfgrpr kavkittmip esvrhyreav kkiegvedsl eadirfamry lidkrlypft vyripvedag rnpgfrvdrv ykvagdpepl aditridlpp mrlvafdiev ysrrgspnpa rdpviivslr dsegkerlie aeghddrrvl refveyvraf dpdiivgyns nhfdwpylme rarrlgikld vtrrvgaept tsvyghvsvq grlnvdlydy aeempeikmk tleevaeylg vmkkservii ewwripeywd dekkrqller yalddvraty glaekmlpfa iqlstvtgvp ldqvgamgvg frlewylmra aydmnelvpn rverrgesyk gavvlkplkg vhenvvvldf ssmypsimik ynvgpdtivd dpsecpkygg cyvapevghr frrsppgffk tvlenllklr rqvkekmkef ppdspeyrly derqkalkvl anasygymgw sharwyckrc aeavtawgrn liltaieyar klglkviygd tdslfvvydk ekvekliefv ekelgfeiki dkiykkvfft eakkryvgll edgridivgf eavrgdwcel akevqekaae ivlntgnvdk aisyirevik qlregkvpit kliiwktlsk rieeyehdap hvmaarrmke agyevspgdk vgyvivkgsg svssraypyf mvdpstidvn yyidhqivpa alrilsyfgv tekqlkaaat vqrslfdffa skk (SEQ ID NO. 97)

ACCESSION BAA81109 ApeI Aeropyrum pernix

mrgstpviil wgrgadgsrv vvfygefrpy fyvlpdgsvg ldqlaamirr lsrpsspils vervrrrfig revealkvtt lvpasvreyr eavrrlggvr dvleadipfa lrfiidfnly pmrwyvaevr evavphgysv draytlsgdi redetriqed plkglrvmaf dievyskmrt pdpkkdpvim iglqqaggei eileaedrsd kkviagfver vksidpdviv gynqnrfdwp ylverarvlg vklavgrrsv epqpglyghy svsgrlnvdl ldfaeelhev kvktleevad ylgvvkiger vtlewwqige ywddpskrei lrkylrddvr stmglaekfl pfgaelsqvs glpldqvmaa svgfrlewrl ireaaklgel vpnrverseg

ryagaivlrp kpgvhediav ldfasmypni mvkynvgpdt lvrpgeeyge eevytapevg hkfrksppgf fkkilerfls wrrqirsemk khppdspeyk llderqkaik llanasygym gwpharwycr ecaeavtawg rsiirtairk agelgleviy gdtdslfvkn dpekverlir fveeelgfdi kvdkvyrrvf fteakkryvg ltvdgkidvv gfeavrgdws elaketqfkv aeivlktgsv deavdyvrni ieklrrgqvd mrklviwktl trppsmyear qphvtaallm eragikvepg akigyvvtkg sgplytrakp yfmaskeevd veyyvdkqvv paalrilqyf gvtekrlkgg grqstlldfm rrgk (SEQ ID NO. 98)

ACCESSION O29753 ARCFU Archaeoglobus fulgidus

mervegwlid adyetiggka vvrlwckddq gifvaydynf dpyfyvigvd edilknaats trreviklks fekaqlktlg revegyivya hhpqhvpklr dylsqfgdvr eadipfayry lidkdlacmd giaiegekqg gvirsykiek veriprmefp elkmlvfdce mlssfgmpep ekdpiivisv ktndddeiil tgderkiisd fvkliksydp diivgynqda fdwpylrkra erwnipldvg rdgsnvvfrg grpkitgrln vdlydiamri sdikikklen vaeflgtkie iadieakdiy rywsrgekek vlnyarqdai ntyliakell pmhyelskmi rlpvddvtrm grgkqvdwll lseakkigei apnppehaes yegafvlepe rglhenvacl dfasmypsim iafnispdty gcrddcyeap evghkfrksp dgffkrilrm liekrrelkv elknlspess eyklldikqq tlkvltnsfy gymgwnlarw ychpcaeatt awgrhfirts akiaesmgfk vlygdtdsif vtkagmtked vdrlidklhe elpiqievde yysaiffvek kryagltedg rlvvkglevr rgdwcelakk vqrevievil keknpekals lvkdvilrik egkvsleevv iykgltkkps kyesmqahvk aalkaremgi iypvsskigy vivkgsgnig draypidlie dfdgenlrik tksgieikkl dkdyyidnqi ipsvlriler fgyteaslkg ssqmsldsff s (SEQ ID NO. 99)

ACCESSION 6435708 Desulfurococcus sp. Tok.

mildadyite dgkpvirvfk kekgefkidy drdfepyiya llkddsaied ikkitaerhg ttvrvtraer vkkkflgrpv evwklyfthp qdvpairdki rehpavvdiy eydipfakry lidrglipme gdeelrmlaf dietlyhege efgegpilmi syadeegarv itwknidlpy vesvstekem ikrflkviqe kdpdvlityn gdnfdfaylk krsemlgvkf ilgrdgsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytletvye pvfgqpkekv yaeeiarawe sgeglervar ysmedakaty elgkeffpme aqlsrlvgqs lwdvsrsstg nlvewfllrk ayerndvapn kpderelarr tesyaggyvk epekglweni vyldykslyp siiithnvsp dtlnregcre ydvapqvghr fckdfpgfip sllgdlleer qkvkkkmkat vdpierklld yrqraikila nsyygyyaya narwycreca esvtawgrqy iettmreiee kfgfkvlyad tdgffatipg adaetvknka keflnyinpr lpglleleye gfyrrgffvt kkkyavidee dkittrglei vrrdwseiak etqarvleai lkhgdveeav rivkevtekl srhevppekl viyeqitrdl rsyratgphv avakrlaarg ikirpgtvis yivlkgpgrv gdraipfdef dpakhrydae yyienqvlpa verilrafgy rkedlryqkt kqaglgawlk pkt (SEQ ID NO. 100)

ACCESSION Q56366 9oN-7

mildtdyite ngkpvirvfk kengefkiey drtfepyfya llkddsaied vkkvtakrhg tvvkvkraek vqkkflgrpi evwklyfnhp qdvpairdri rahpavvdiy eydipfakry lidkglipme gdeeltmlaf dietlyhege efgtgpilmi syadgsearv itwkkidlpy vdvvstekem ikrflrvvre kdpdvlityn gdnfdfaylk krceelgikf tlgrdgsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye avfgkpkekv yaeeiaqawe sgeglervar ysmedakvty elgreffpme aqlsrligqs lwdvsrsstg nlvewfllrk aykrnelapn kpderelarr rggyaggyvk eperglwdni vyldfrslyp siiithnvsp dtlnregcke ydvapevghk fckdfpgfip sllgdlleer qkikrkmkat vdplekklld yrqraikila nsfygyygya karwyckeca esvtawgrey iemvirelee kfgfkvlyad tdglhatipg adaetvkkka keflkyinpk lpglleleye gfyvrgffvt kkkyavidee gkittrglei vrrdwseiak etqarvleai lkhgdveeav

rivkevtekl skyevppekl viheqitrdl rdykatgphv avakrlaarg vkirpgtvis yivlkgsgri gdraipadef dptkhrydae yyienqvlpa verilkafgy rkedlryqkt kqvglgawlk vkgkk (SEQ ID NO. 101)

ACCESSION O29753 Afu

mervegwlid adyetiggka vvrlwckddq gifvaydynf dpyfyvigvd edilknaats trreviklks fekaqlktlg revegyivya hhpqhvpklr dylsqfgdvr eadipfayry lidkdlacmd giaiegekqg gvirsykiek veriprmefp elkmlvfdce mlssfgmpep ekdpiivisv ktnddeiil tgderkiisd fvkliksydp diivgynqda fdwpylrkra erwnipldvg rdgsnvvfrg grpkitgrln vdlydiamri sdikikklen vaeflgtkie iadieakdiy rywsrgekek vlnyarqdai ntyliakell pmhyelskmi rlpvddvtrm grgkqvdwll lseakkigei apnppehaes yegafvlepe rglhenvacl dfasmypsim iafnispdty gcrddcyeap evghkfrksp dgffkrilrm liekrrelkv elknlspess eyklldikqq tlkvltnsfy gymgwnlarw ychpcaeatt awgrhfirts akiaesmgfk vlygdtdsif vtkagmtked vdrlidklhe elpiqievde yysaiffvek kryagltedg rlvvkglevr rgdwcelakk vqrevievil keknpekals · lvkdvilrik egkvsleevv iykgltkkps kyesmqahvk aalkaremgi iypvsskigy vivkgsgnig draypidlie dfdgenlrik tksgieikkl dkdyyidnqi ipsvlriler fgyteaslkg ssqmsldsff s (SEQ ID NO. 102)

ACCESSION P52025 Mvo

mdldynskdl cidmyykncg lkkpeinlqk ecefkpyfyv dtsepkeiyd yldglnqeid lkklepefen ntslkvqdli tnieiiekiv ysdyilngkd isevsdfknk kerkickvyv kypnhvkiir eyfkefgksy efdipflrry midqdivpsa kysednkidn sipelnciaf dmelyckkep nakkdpiimv nlfskdyqkv itykkfense yngcvdyvkd ekeliqktie ilkqydviyt yngdnfdfpy lkkraniyei eldfdnasns qqpqiikisk gginrkskip giihidlypi arkllnltky klenvvqelf kinkeavdyg dipkmweted ttllryayed alytykmgny flpleimfsr ivnqplydts rmnssqmvef lllkrsfeqn mispnrpsss syrerakfsy eggyvreplk giqedivsld fmslypsili shnispetvi yeekerenme lgiipktlne llsrrkhikm llkdkiqkne fdeeysrleh eqksikvlan shygylafpm arwysdkcae mvtglgrkyi qetiekaeef gfkviyadtd gfyakwdydk lqkgkkeend ksdklsnlpk lskeeliilt kkflkginee lpegmelefe ghfkrglfvt kkkyaliedd ghivvkglev vrrdwsniak dtqqaviral ledgdvnlak kiikntidnl kkgnidkndl lihtqltkni eeykstaphi evakkikqrg dsvrvgdvis yiivkgsrsi seraelleya gdydinyyid nqvlppviri meslgisede lknsgkqfkl dqfm (SEQ ID NO. 103)

ACCESSION AAF27815

melkvwpldi tyavvgsvpe irifgilssg ervvlidrsf kpyfyvdcav cepaalktal srvapiddvq iverrflgrs kkflkviaki pedvrklrea amsiprvsgv yeadirfymr ymidmgvvpc swnvaeveeg grlggiptyv vsqwygideg fppslkvmaf dievynergs pdpirdpvvm laiktndghe evfeasgkdd rgvvrafvdf irsydpdviv gynsngfdwp ylverakavg vplkvdrlsn ppqqsvyghw sivgranvdl yniveefpei klktldrvae yfgvmkreer vlipghkiye ywkdpnkrpl lkryvlddvr stlgladkll pfliqlssvs glpldqvaaa svgnrvewml lryayrlgev apnreereye pykgaivlep kpgmyedvlv ldfssmypni mmkynlspdt ylepgepdpp egvnvapevg hrfrrsppgf vpqvlkslve lrkavreeak kyppdspefk ilderqralk vmanaiygyl gwvgarwykr evaesvtafa railkdvieq arrlgivvvy gdtdslfvkk hgdvdkliky veekygidik vdkdyakvlf teakkryagl lrdgridivg fevvrgdwse lakdvqlrvi eiilksrdiv earhgvikyi reiierlkny kfniddliiw ktldkeldey kaypphvhaa qilkrhgyrv gkgttigyvi vkggekvser alpyillddi kkididyyie rqiipaalri aevigvkesd lktgrmersl ldfls (SEQ ID NO. 104)

ACCESSION AAC62712 Csy

mtvqdaveip psllvsatyd sqagavvlkf yepesqkivh wtdntghkpy cytrqppsel gelegredvl gteqvmrhdl iadkdvpvtk itvadplaig gtnseksirn imdtwesdik yyenylydks lvvgryysvs ggkviphdmp isdevklalk sllwdkvvde gmadrkefre fiagwadlln qpiprirrls fdievdseeg ripdpkisdr rvtavgfaat dglkqvfvlr sgaeegengv tpgvevvfyd keadmirdal svigsypfvl tyngddfdmp ymlnrarrlg vsdsdiplym mrdsatlrhg vhldlyrtfs nrsfqlyafa akytdyslns vtkamlgegk vdygvklgdl tlyqtanycy hdarltlels tfgneilmdl lvvtsriarm piddmsrmgv sqwirsllyy ehrqrnalip rrdelegrsr evsndavikd kkfrgglvve peegihfdvt vmdfaslyps iikvrnlsye tvrcvhaeck kntipdtnhw vctknnglts miigslrdlr vnyykslsks tsiteeqrqq ytvisqalkv vlnasygvmg aeifplyflp aaeattavgr yiimqtishc eqmgvrvlyg dtdslfikdp eerqiheive hakkehgvel evdkeyryvv lsnrkknyfg vtragkvdvk gltgkkshtp pfikelfysl ldilsgvese defesakmri skaiaacgkr leerqiplvd lafnvmiska pseyvktvpq hiraarllen arevkkgdii syvkvmnktg vkpvemarag evdtskylef mestldqlts smgldfdeil gkpkqtgmeq fffk (SEQ ID NO. 105)

ACCESSION P95690 Sac

mskqatlfdf sikkneskeq tnqesvevpk qtanrtkiew ikeaedgkvy fllqvdydgk ksravcklyd kegkkiyimq desghkpyfl tdidpdkvnk itkvvrdpsf dhlelinkvd pytgkkirlt kivvkdplav rrmrsslpka yeahikyynn yvydnglipg liykvnkgkl tqlnpelkge eineikklsd ayemtketvn dwipiletev pdikrvsldi evytpnrgri pdperaefpi isvalagndg skivlalkre dvnsdfskkd gvqveifdse kkllarlfei ireypmlltf ngddfdipyi yfralrlnfs peevpldvvs gegkflagih idlykfffnr avsiyafegk yseyslyava tallgiskvk ldtfisfmdi dklieynlrd aeitlklttf nnnlvlklmv llarisklgl eeltrtevst wiknlyyweh rkrnwliplk eeilvrsnqv ktaavikgkk ykgavvidpp agvyfnvvvl dfaslypsii knwnisyeti eidectkkvw vedetgeklh yvcmdkpgit avyqglirdf rvkvykkkak ysniseeqrs lydvvqramk vfinatygvf gaenfplyap avaesvtaig ryiitttykq aeklnlkviy gdtdslflyn ptkdkleeli kfvkqnfnld levdntykyv aysglkknyf gvypdgktei kgmlakkrnt pefikkefae iknmlaslns pndipevknk leikikdiyy klrnkgynld dlafrimlsk pldsytkntp qhvkaglqlr afgvnvlprd vimfvkvksk dgvkayqlak iseidiekyv etlrttfeqi lkafgiswde ivstisidsf fgskk (SEQ ID NO. 106)

ACCESSION BAA23994 Soh

marqitlfdf tlkkeqnkde srkeeiphan ineerrkpke wikeaeegks yfllqvdydg kkskaickly dketkkiyil ydntghkpyf ltdidpekvn kipkvvrdps fdhletviki dpysgnkikl tkivvkdpla vrrmrnsvpk ayeahikyfn nyiydlglip glpyvvkkgk leqlrpelkg eevdeirkaf adsdemtkea vndwipifes evpdvkrvai dievytpikg ripdpekaef piisislagn dgtkrvlvll redvnsqitk hdvivetfks erelirrffd iildypiilt fngddfdipy iyyralklnf tpeeipfdii ndegkylagi hidlykfffn rairnyafeg kyneynldav atallgmskv kldtlisfld ldklieynsr daeitlkltt fnnnlvwkli illariskmg leeltrtevs twiknlyywe hrrrnwlipl keeiltrssq iktaaiikgk rykgavvidp pagvffnvvv ldfaslypsi irnwnisyet vdvencknke yvrdetgevl hyickdkpgi tavitgllrd frvkvykkka ksqniseeqr svydvvqram kvfinatygv fgaenfplya pavaesvtai gryvitttvn ycrsiglqvl ygdtdsmflw npskekleei ikfvkgkfgl dlevdkvykf vafsglkkny lgvypdgktd ikgmlakkrn tpefikkefn evkqlvttin spddipkird qleykikeiy eklrhkgynl delafrvmls kplesytknt pqhvkaalql rsygvmvlpr diimfvkvks kdgvkpvqla klseidvdky idavrstfeq ilkafgliga nllqllsils lt (SEQ ID NO. 107)

ACCESSION P26811 Sso

mtkqltlfdi psskpakseq ntqqsqqsap veekkvvrre wleeaqenki yfllqvdydg kkgkavcklf dketqkiyal ydntghkpyf lvdlepdkvg kipkivrdps fdhietvski dpytwnkfkl tkivvrdpla vrrlrndvpk ayeahikyfn nymydiglip gmpyvvkngk lesvylslde kdveeikkaf adsdemtrqm avdwlpifet eipkikrvai dievytpvkg ripdsqkaef piisialags dglkkvlvln rndvnegsvk ldgisverfn teyellgrff dilleypivl tfngddfdlp yiyfralklg yfpeeipidv agkdeakyla glhidlykff fnkavrnyaf egkyneynld avakallgts kvkvdtlisf ldveklieyn frdaeitlql ttfnndltmk livlfsrisr lgieeltrte istwvknlyy wehrkrnwli plkeeilaks snirtsalik gkgykgavvi dppagiffni tvldfaslyp siirtwnlsy etvdiqqckk pyevkdetge vlhivcmdrp gitavitgll rdfrvkiykk kaknpnnsee qkllydvvqr amkvfinaty gvfgaetfpl yapavaesvt algryvitst vkkareeglt vlygdtdslf llnppknsle niikwvkttf nldlevdkty kfvafsglkk nyfgvyqdgk vdikgmlvkk rntpefvkkv fnevkelmis inspndvkei krkivdvvkg syeklknkgy nldelafkvm lskpldaykk ntpqhvkaal qlrpfgvnvl prdiiyyvkv rskdgvkpvq lakvteidae kylealrstf eqilrafgvs wdeiaatmsi dsffsypskg ns (SEQ ID NO. 108)

Please note that only upper-case letters are considered to be aligned.

Figure 7B

Alignment (DIALIGN format):

```
Pfu          1   MILDVDYITE EGKPVIRLFK KENGKFKIEH DRTFRPYIYA LLRDDSKIEE
Tgo          1   MILDTDYITE DGKPVIRIFK KENGEFKIDY DRNFEPYIYA LLKDDSAIED
KOD          1   MILDTDYITE DGKPVIRIFK KENGEFKIEY DRTFEPYFYA LLKDDSAIEE
Vent         1   MILDTDYITK DGKPIIRIFK KENGEFKIEL DPHFQPYIYA LLKDDSAIEE
Deep         1   MILDADYITE DGKPIIRIFK KENGEFKVEY DRNFRPYIYA LLKDDSQIDE
JDF-3        1   MILDVDYITE NGKPVIRVFK KENGEFRIEY DREFEPYFYA LLRDDSAIEE

                                                          V93
Pfu         51   VKKITGERHG KIVRIVDVEK VEKKFLGKPI TVWKLYLEHP QDVPTIREKV
Tgo         51   VKKITAERHG TTVRVVRAEK VKKKFLGRPI EVWKLYFTHP QDVPAIRDKI
KOD         51   VKKITAERHG TVVTVKRVEK VQKKFLGRPV EVWKLYFTHP QDVPAIRDKI
Vent        51   IKAIKGERHG KTVRVLDAVK VRKKFLGREV EVWKLIFEHP QDVPAMRGKI
Deep        51   VRKITAERHG KIVRIIDAEK VRKKFLGRPI EVWRLYFEHP QDVPAIRDKI
JDF-3       51   IKKITAERHG RVVKVKRAEK VKKKFLGRSV EVWVLYFTHP QDVPAIRDKI

                                                    DXE (exo I)
Pfu        101   REHPAVVDIF EYDIPFAKRY LIDKGLIPME GEEELKILAF DIETLYHEGE
Tgo        101   KEHPAVVDIY EYDIPFAKRY LIDKGLIPME GDEELKMLAF DIETLYHEGE
KOD        101   REHGAVIDIY EYDIPFAKRY LIDKGLVPME GDEELKMLAF DIQTLYHEGE
Vent       101   REHPAVVDIY EYDIPFAKRY LIDKGLIPME GDEELKLLAF DIETFYHEGD
Deep       101   REHSAVIDIF EYDIPFAKRY LIDKGLIPME GDEELKLLAF DIETLYHEGE
JDF-3      101   RKHPAVIDIY EYDIPFAKRY LIDKGLIPME GEEELKLMSF DIETLYHEGE
                           101        121        131        141 -143

Pfu        151   EFGKGPIIMI SYADENEAKV ITWKNIDLPY VEVVSSEREM IKRFLRIIRE
Tgo        151   EFAEGPILMI SYADEEGARV ITWKNIDLPY VDVVSTEKEM IKRFLKVVKE
KOD        151   EFAEGPILMI SYADEEGARV ITWKNVDLPY VDVVSTEREM IKRFLRVVKE
Vent       151   EFGKGEIIMI SYADEEEARV ITWKNIDLPY VDVVSNEREM IKRFvQVVKE
Deep       151   EFAKGPIIMI SYADEEEAKV ITWKKIDLPY VEVVSSEREM IKRFLKVIRE
JDF-3      151   EFGTGPILMI SYADESEARV ITWKKIDLPY VEVVSTEKEM IKRFLRVVKE

                                 NX2-3FD (exo II)
Pfu        201   KDPDIIVTYN GDSFDFPYLA KRAEKLGIKL TIGRDGS--E PKMQRIGDMT
Tgo        201   KDPDVLITYN GDNFDFAYLK KRSEKLGVKF ILGREGS--E PKIQRMGDRF
KOD        201   KDPDVLITYN GDNFDFAYLK KRCEKLGINF ALGRDGS--E PKIQRMGDRF
Vent       201   KDPDVIITYN GDNFDLPYLI KRAEKLGVRL VLGRDkehpE PKIQRMGDSF
Deep       201   KDPDVIITYN GDSFDLPYLV KRAEKLGIKL PLGRDGS--E PKMQRLGDMT
JDF-3      201   KDPDVLITYN GDNFDFAYLK KRCEKLGVSF TLGRDGS--E PKIQRMGDRF
                           210 -215             231        239

Pfu        249   AVEVKGRIHF DLYHVITRTI NLPTYTLEAV YEAIFGKPKE KVYADEIAKA
Tgo        249   AVEVKGRIHF DLYPVIRRTI NLPTYTLEAV YEAIFGQPKE KVYAEEIAQA
KOD        249   AVEVKGRIHF DLYPVIRRTI NLPTYTLEAV YEAVFGQPKE KVYAEEITPA
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Vent    251  AVEIKGRIHF DLFPVVRRTI NLPTYTLEAV YEAVLGKTKS KLGAEEIAAI
Deep    249  AVEIKGRIHF DLYHVIRRTI NLPTYTLEAV YEAIFGKPKE KVYAHEIAEA
JDF-3   249  AVEVKGRVHF DLYPVIRRTI NLPTYTLEAV YEAVFGKPKE KVYAEEIATA

                                  YX3D (exo III)
Pfu     299  WESGENLERV AKYSMEDAKA TYELGKEFLP MEIQLSRLVG QPLWDVSRSS
Tgo     299  WETGEGLERV ARYSMEDAKV TYELGKEFFP MEAQLSRLVG QSLWDVSRSS
KOD     299  WETGENLERV ARYSMEDAKV TYELGKEFLP MEAQLSRLIG QSLWDVSRSS
Vent    301  WETEESMKKL AQYSMEDARA TYELGKEFFP MEAELAKLIG QSVWDVSRSS
Deep    299  WETGKGLERV AKYSMEDAKV TYELGREFFP MEAQLSRLVG QPLWDVSRSS
JDF-3   299  WETGEGLERV ARYSMEDARV TYELGREFFP MEAQLSRLIG QGLWDVSRSS
                                  311-315

Pfu     349  TGNLVEWFLL RKAYERNEVA PNKPSEEEYQ RRLRESYTGG FVKEPEKGLW
Tgo     349  TGNLVEWFLL RKAYERNELA PNKPDERELA RR-RESYAGG YVKEPERGLW
KOD     349  TGNLVEWFLL RKAYERNELA PNKPDEKELA RR-RQSYEGG YVKEPERGLW
Vent    351  TGNLVEWYLL RVAYARNELA PNKPDEEEYK RRLRTTYLGG YVKEPEKGLW
Deep    349  TGNLVEWYLL RKAYERNELA PNKPDEREYE RRLRESYAGG YVKEPEKGLW
JDF-3   349  TGNLVEWFLL RKAYERNELA PNKPDERELA RR-RggYAGG YVKEPERGLW

Pfu     399  ENIVYLDFRA LYPSIIITHN VSPDTLNLEG CKNYDIAPQV GHKFCKDIPG
Tgo     398  ENIVYLDFRS LYPSIIITHN VSPDTLNREG CEEYDVAPQV GHKFCKDFPG
KOD     398  ENIVYLDFRS LYPSIIITHN VSPDTLNREG CKEYDVAPQV GHRFCKDFPG
Vent    401  ENIIYLDFRS LYPSIIVTHN VSPDTLEKEG CKNYDVAPIV GYRFCKDFPG
Deep    399  EGLVSLDFRS LYPSIIITHN VSPDTLNREG CREYDVAPEV GHKFCKDFPG
JDF-3   398  DNIVYLDFRS LYPSIIITHN VSPDTLNREG CRSYDVAPEV GHKFCKDFPG

Pfu     449  FIPSLLGHLL EERQKIKTKM KETQDPIEKI LLDYRQKAIK LLANSFYGYY
Tgo     448  FIPSLLGDLL EERQKVKKKM KATIDPIEKK LLDYRQRAIK ILANSFYGYY
KOD     448  FIPSLLGDLL EERQKIKKKM KATIDPIERK LLDYRQRAIK ILANSYYGYY
Vent    451  FIPSILGDLI AMRQDIKKKM KSTIDPIEKK MLDYRQRAIK LLANSYYGYM
Deep    449  FIPSLLKRLL DERQEIKRKM KASKDPIEKK MLDYRQRAIK ILANSYYGYY
JDF-3   448  FIPSLLGNLL EERQKIKRKM KATLDPLEKN LLDYRQRAIK ILANSYYGYY

Pfu     499  GYAKARWYCK ECAESVTAWG RKYIELVWKE LEEKFGFKVL YIDTDGLYAT
Tgo     498  GYAKARWYCK ECAESVTAWG RQYIETTIRE IEEKFGFKVL YADTDGFFAT
KOD     498  GYARARWYCK ECAESVTAWG REYITMTIKE IEEKYGFKVI YSDTDGFFAT
Vent    501  GYPKARWYSK ECAESVTAWG RHYIEMTIRE IEEKFGFKVL YADTDGFYAT
Deep    499  GYAKARWYCK ECAESVTAWG REYIEFVRKE LEEKFGFKVL YIDTDGLYAT
JDF-3   498  GYARARWYCR ECAESVTAWG REYIEMVIRE LEEKFGFKVL YADTDGLHAT

Pfu     549  IPGGESEEIK KKALEFVKYI NSKLPGLLEL EYEGFYKRGF FVTKKRYAVI
Tgo     548  IPGADAETVK KKAKEFLDYI NAKLPGLLEL EYEGFYKRGF FVTKKKYAVI
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KOD          548   IPGADAETVK KKAMEFLNYI NAKLPGALEL EYEGFYKRGF FVTKKKYAVI
Vent         551   IPGEKPELIK KKAKEFLNYI NSKLPGLLEL EYEGFYLRGF FVTKKRYAVI
Deep         549   IPGAKPEEIK KKALEFVDYI NAKLPGLLEL EYEGFYVRGF FVTKKKYALI
JDF-3        548   IPGADAETVK KKAMEFLNYI NPKLPGLLEL EYEGFYVRGF FVTKKKYAVI

Pfu          599   DEEGKVITRG LEIVRRDWSE IAKETQARVL ETILKHGDVE EAVRIVKEVI
Tgo          598   DEEDKITTRG LEIVRRDWSE IAKETQARVL EAILKHGDVE EAVRIVKEVT
KOD          598   DEEGKITTRG LEIVRRDWSE IAKETQARVL EALLKDGDVE KAVRIVKEVT
Vent         601   DEEGRITTRG LEVVRRDWSE IAKETQAKVL EAILKEGSVE KAVEVVRDVV
Deep         599   DEEGKIITRG LEIVRRDWSE IAKETQAKVL EAILKHGNVE EAVKIVKEVT
JDF-3        598   DEEGKITTRG LEIVRRDWSE IAKETQARVL EAILRHGDVE EAVRIVREVT

Pfu          649   QKLANYEIPP EKLAIYEQIT RPLHEYKAIG PHVAVAKKLA AKGVKIKPGM
Tgo          648   EKLSKYEVPP EKLVIYEQIT RDLKDYKATG PHVAVAKRLA ARGIKIRPGT
KOD          648   EKLSKYEVPP EKLVIHEQIT RDLKDYKATG PHVAVAKRLA ARGVKIRPGT
Vent         651   EKIAKYRVPL EKLVIHEQIT RDLKDYKAIG PHVAIAKRLA ARGIKVKPGT
Deep         649   EKLSKYEIPP EKLVIYEQIT RPLHEYKAIG PHVAVAKRLA ARGVKVRPGM
JDF-3        648   EKLSKYEVPP EKLVIHEQIT RELKDYKATG PHVAIAKRLA ARGVKIRPGT

Pfu          699   VIGYIVLRGD GPISNRAILA EEYDPKKHKY DAEYYIENQV LPAVLRILEG
Tgo          698   VISYIVLKGS GRIGDRAIPF DEFDPAKHKY DAEYYIENQV LPAVERILRA
KOD          698   VISYIVLKGS GRIGDRAIPF DEFDPTKHKY DAEYYIENQV LPAVERILRA
Vent         701   IISYIVLKGS GKISDRVILL TEYDPRKHKY DPDYYIENQV LPAVLRILEA
Deep         699   VIGYIVLRGD GPISKRAILA EEFDLRKHKY DAEYYIENQV LPAVLRILEA
JDF-3        698   VISYIVLKGS GRIGDRAIPF DEFDPTKHKY DADYYIENQV LPAVERILRA

Pfu          749   FGYRKEDLRY QKTRQVGLTS WLNIKKs--
Tgo          748   FGYRKEDLRY QKTRQVGLGA WLKPKt---
KOD          748   FGYRKEDLRY QKTRQVGLSA WLKPKGt--
Vent         751   FGYRKEDLRY QSSKQTGLDA WLKr-----
Deep         749   FGYRKEDLRW QKTKQTGLTA WLNIKKk--
JDF-3        748   FGYRKEDLRY QKTRQVGLGA WLKPKGkkk
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Alignment (FASTA format):

```
>Pfu
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEE
VKKITGERHGKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKV
REHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGE
EFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIRE
KDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS--EPKMQRIGDMT
AVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKA
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WESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSS
TGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLW
ENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPG
FIPSLLGHLLEERQKIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYY
GYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYAT
IPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVI
DEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVI
QKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPGM
VIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEG
FGYRKEDLRYQKTRQVGLTSWLNIKKs—

>Tgo
MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIED
VKKITAERHGTTVRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKI
KEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGE
EFAEGPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKE
KDPDVLITYNGDNFDFAYLKKRSEKLGVKFILGREGS—EPKIQRMGDRF
AVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQA
WETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDERELARR-RESYAGGYVKEPERGLW
ENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPG
FIPSLLGDLLEERQKVKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYY
GYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFAT
IPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVI
DEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVT
EKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRA
FGYRKEDLRYQKTRQVGLGAWLKPKt——

>KOD
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEE
VKKITAERHGTVVTVKRVEKVQKKFLGRPVEVWKLYFTHPQDVPAIRDKI
REHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGE
EFAEGPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKE
KDPDVLITYNGDNFDFAYLKKRCEKLGINFALGRDGS—EPKIQRMGDRF
AVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPA
WETGENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDEKELARR-RQSYEGGYVKEPERGLW
ENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPG
FIPSLLGDLLEERQKIKKKMKATIDPIERKLLDYRQRAIKILANSYYGYY
GYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYSDTDGFFAT
IPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVI
DEEGKITTRGLEIVRRDWSEIAKETQARVLEALLKDGDVEKAVRIVKEVT
EKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRA
FGYRKEDLRYQKTRQVGLSAWLKPKGt—

>Vent
MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEE
IKAIKGERHGKTVRVLDAVKVRKKFLGREVEVWKLIFEHPQDVPAMRGKI
REHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGD
EFGKGEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFvQVVKE
KDPDVIITYNGDNFDLPYLIKRAEKLGVRLVLGRDkehpEPKIQRMGDSF
AVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAI
WETEESMKKLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSS
TGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRTTYLGGYVKEPEKGLW
ENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPG
FIPSILGDLIAMRQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYM
GYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKVLYADTDGFYAT

IPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVI
DEEGRITTRGLEVVRRDWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVV
EKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARGIKVKPGT
IISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEA
FGYRKEDLRYQSSKQTGLDAWLKr———

>Deep
MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDE
VRKITAERHGKIVRIIDAEKVRKKFLGRPIEVWRLYFEHPQDVPAIRDKI
REHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGE
EFAKGPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIRE
KDPDVIITYNGDSFDLPYLVKRAEKLGIKLPLGRDGS—EPKMQRLGDMT
AVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEA
WETGKGLERVAKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSS
TGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESYAGGYVKEPEKGLW
EGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPG
FIPSLLKRLLDERQEIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYY
GYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLYIDTDGLYAT
IPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALI
DEEGKIITRGLEIVRRDWSEIAKETQAKVLEAILKHGNVEEAVKIVKEVT
EKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVKVRPGM
VIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEA
FGYRKEDLRWQKTKQTGLTAWLNIKKk—

>JDF-3
MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEE
IKKITAERHGRVVKVKRAEKVKKKFLGRSVEVWVLYFTHPQDVPAIRDKI
RKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGE
EFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKE
KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGS—EPKIQRMGDRF
AVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATA
WETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDERELARR-RggYAGGYVKEPERGLW
DNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPG
FIPSLLGNLLEERQKIKRKMKATLDPLEKNLLDYRQRAIKILANSYYGYY
GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHAT
IPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVI
DEEGKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVT
EKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRA
FGYRKEDLRYQKTRQVGLGAWLKPKGkkk

Sequence tree:
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Tree constructed using UPGMA

(((Pfu :0.000998,
Deep :0.000998):0.000080,
((Tgo :0.000905,
KOD :0.000905):0.000032,
JDF-3 :0.000937):0.000141):0.000067,
Vent :0.001144);

Please note that only upper-case letters are considered to be aligned.

Alignment (DIALIGN format):

```
Pfu          1  MILDVDYITE EGKPVIRLFK KENGKFKIEH DRTFRPYIYA LLRDDSKIEE
Tgo          1  MILDTDYITE DGKPVIRIFK KENGEFKIDY DRNFEPYIYA LLKDDSAIED
KOD          1  MILDTDYITE DGKPVIRIFK KENGEFKIEY DRTFEPYFYA LLKDDSAIEE
Vent         1  MILDTDYITK DGKPIIRIFK KENGEFKIEL DPHFQPYIYA LLKDDSAIEE
Deep         1  MILDADYITE DGKPIIRIFK KENGEFKVEY DRNFRPYIYA LLKDDSQIDE
JDF-3        1  MILDVDYITE NGKPVIRVFK KENGEFRIEY DREFEPYFYA LLRDDSAIEE

Pfu         51  VKKITGERHG KIVRIVDVEK VEKKFLGKPI TVWKLYLEHP QDVPTIREKV
Tgo         51  VKKITAERHG TTVRVVRAEK VKKKFLGRPI EVWKLYFTHP QDVPAIRDKI
KOD         51  VKKITAERHG TVVTVKRVEK VQKKFLGRPV EVWKLYFTHP QDVPAIRDKI
Vent        51  IKAIKGERHG KTVRVLDAVK VRKKFLGREV EVWKLIFEHP QDVPAMRGKI
Deep        51  VRKITAERHG KIVRIIDAEK VRKKFLGRPI EVWRLYFEHP QDVPAIRDKI
JDF-3       51  IKKITAERHG RVVKVKRAEK VKKKFLGRSV EVWVLYFTHP QDVPAIRDKI

Pfu        101  REHPAVVDIF EYDIPFAKRY LIDKGLIPME GEEELKILAF DIETLYHEGE
Tgo        101  KEHPAVVDIY EYDIPFAKRY LIDKGLIPME GDEELKMLAF DIETLYHEGE
KOD        101  REHGAVIDIY EYDIPFAKRY LIDKGLVPME GDEELKMLAF DIQTLYHEGE
Vent       101  REHPAVVDIY EYDIPFAKRY LIDKGLIPME GDEELKLLAF DIETFYHEGD
Deep       101  REHSAVIDIF EYDIPFAKRY LIDKGLIPME GDEELKLLAF DIETLYHEGE
JDF-3      101  RKHPAVIDIY EYDIPFAKRY LIDKGLIPME GEEELKLMSF DIETLYHEGE

Pfu        151  EFGKGPIIMI SYADENEAKV ITWKNIDLPY VEVVSSEREM IKRFLRIIRE
Tgo        151  EFAEGPILMI SYADEEGARV ITWKNIDLPY VDVVSTEKEM IKRFLKVVKE
KOD        151  EFAEGPILMI SYADEEGARV ITWKNVDLPY VDVVSTEREM IKRFLRVVKE
Vent       151  EFGKGEIIMI SYADEEEARV ITWKNIDLPY VDVVSNEREM IKRFvQVVKE
Deep       151  EFAKGPIIMI SYADEEEAKV ITWKKIDLPY VEVVSSEREM IKRFLKVIRE
JDF-3      151  EFGTGPILMI SYADESEARV ITWKKIDLPY VEVVSTEKEM IKRFLRVVKE

Pfu        201  KDPDIIVTYN GDSFDFPYLA KRAEKLGIKL TIGRDGS--E PKMQRIGDMT
Tgo        201  KDPDVLITYN GDNFDFAYLK KRSEKLGVKF ILGREGS--E PKIQRMGDRF
KOD        201  KDPDVLITYN GDNFDFAYLK KRCEKLGINF ALGRDGS--E PKIQRMGDRF
Vent       201  KDPDVIITYN GDNFDLPYLI KRAEKLGVRL VLGRDkehpE PKIQRMGDSF
Deep       201  KDPDVIITYN GDSFDLPYLV KRAEKLGIKL PLGRDGS--E PKMQRLGDMT
JDF-3      201  KDPDVLITYN GDNFDFAYLK KRCEKLGVSF TLGRDGS--E PKIQRMGDRF

Pfu        249  AVEVKGRIHF DLYHVITRTI NLPTYTLEAV YEAIFGKPKE KVYADEIAKA
Tgo        249  AVEVKGRIHF DLYPVIRRTI NLPTYTLEAV YEAIFGQPKE KVYAEEIAQA
KOD        249  AVEVKGRIHF DLYPVIRRTI NLPTYTLEAV YEAVFGQPKE KVYAEEITPA
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Vent    251  AVEIKGRIHF DLFPVVRRTI NLPTYTLEAV YEAVLGKTKS KLGAEEIAAI
Deep    249  AVEIKGRIHF DLYHVIRRTI NLPTYTLEAV YEAIFGKPKE KVYAHEIAEA
JDF-3   249  AVEVKGRVHF DLYPVIRRTI NLPTYTLEAV YEAVFGKPKE KVYAEEIATA

Pfu     299  WESGENLERV AKYSMEDAKA TYELGKEFLP MEIQLSRLVG QPLWDVSRSS
Tgo     299  WETGEGLERV ARYSMEDAKV TYELGKEFFP MEAQLSRLVG QSLWDVSRSS
KOD     299  WETGENLERV ARYSMEDAKV TYELGKEFLP MEAQLSRLIG QSLWDVSRSS
Vent    301  WETEESMKKL AQYSMEDARA TYELGKEFFP MEAELAKLIG QSVWDVSRSS
Deep    299  WETGKGLERV AKYSMEDAKV TYELGREFFP MEAQLSRLVG QPLWDVSRSS
JDF-3   299  WETGEGLERV ARYSMEDARV TYELGREFFP MEAQLSRLIG QGLWDVSRSS

Pfu     349  TGNLVEWFLL RKAYERNEVA PNKPSEEEYQ RRLRESYTGG FVKEPEKGLW
Tgo     349  TGNLVEWFLL RKAYERNELA PNKPDERELA RR-RESYAGG YVKEPERGLW
KOD     349  TGNLVEWFLL RKAYERNELA PNKPDEKELA RR-RQSYEGG YVKEPERGLW
Vent    351  TGNLVEWYLL RVAYARNELA PNKPDEEEYK RRLRTTYLGG YVKEPEKGLW
Deep    349  TGNLVEWYLL RKAYERNELA PNKPDEREYE RRLRESYAGG YVKEPEKGLW
JDF-3   349  TGNLVEWFLL RKAYERNELA PNKPDERELA RR-RggYAGG YVKEPERGLW

                    DXXSLYPSII (Region II)
Pfu     399  ENIVYLDFRA LYPSIIITHN VSPDTLNLEG CKNYDIAPQV GHKFCKDIPG
Tgo     398  ENIVYLDFRS LYPSIIITHN VSPDTLNREG CEEYDVAPQV GHKFCKDFPG
KOD     398  ENIVYLDFRS LYPSIIITHN VSPDTLNREG CKEYDVAPQV GHRFCKDFPG
Vent    401  ENIIYLDFRS LYPSIIVTHN VSPDTLEKEG CKNYDVAPIV GYRFCKDFPG
Deep    399  EGLVSLDFRS LYPSIIITHN VSPDTLNREG CREYDVAPEV GHKFCKDFPG
JDF-3   398  DNIVYLDFRS LYPSIIITHN VSPDTLNREG CRSYDVAPEV GHKFCKDFPG

Pfu     449  FIPSLLGHLL EERQKIKTKM KETQDPIEKI LLDYRQKAIK LLANSFYGYY
Tgo     448  FIPSLLGDLL EERQKVKKKM KATIDPIEKK LLDYRQRAIK ILANSFYGYY
KOD     448  FIPSLLGDLL EERQKIKKKM KATIDPIERK LLDYRQRAIK ILANSYYGYY
Vent    451  FIPSILGDLI AMRQDIKKKM KSTIDPIEKK MLDYRQRAIK LLANSYYGYM
Deep    449  FIPSLLKRLL DERQEIKRKM KASKDPIEKK MLDYRQRAIK ILANSYYGYY
JDF-3   448  FIPSLLGNLL EERQKIKRKM KATLDPLEKN LLDYRQRAIK ILANSYYGYY

Pfu     499  GYAKARWYCK ECAESVTAWG RKYIELVWKE LEEKFGFKVL YIDTDGLYAT
Tgo     498  GYAKARWYCK ECAESVTAWG RQYIETTIRE IEEKFGFKVL YADTDGFFAT
KOD     498  GYARARWYCK ECAESVTAWG REYITMTIKE IEEKYGFKVI YSDTDGFFAT
Vent    501  GYPKARWYSK ECAESVTAWG RHYIEMTIRE IEEKFGFKVL YADTDGFYAT
Deep    499  GYAKARWYCK ECAESVTAWG REYIEFVRKE LEEKFGFKVL YIDTDGLYAT
JDF-3   498  GYARARWYCR ECAESVTAWG REYIEMVIRE LEEKFGFKVL YADTDGLHAT

Pfu     549  IPGGESEEIK KKALEFVKYI NSKLPGLLEL EYEGFYKRGF FVTKKRYAVI
Tgo     548  IPGADAETVK KKAKEFLDYI NAKLPGLLEL EYEGFYKRGF FVTKKKYAVI
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```
KOD          548   IPGADAETVK KKAMEFLNYI NAKLPGALEL EYEGFYKRGF FVTKKKYAVI
Vent         551   IPGEKPELIK KKAKEFLNYI NSKLPGLLEL EYEGFYLRGF FVTKKRYAVI
Deep         549   IPGAKPEEIK KKALEFVDYI NAKLPGLLEL EYEGFYVRGF FVTKKKYALI
JDF-3        548   IPGADAETVK KKAMEFLNYI NPKLPGLLEL EYEGFYVRGF FVTKKKYAVI

Pfu          599   DEEGKVITRG LEIVRRDWSE IAKETQARVL ETILKHGDVE EAVRIVKEVI
Tgo          598   DEEDKITTRG LEIVRRDWSE IAKETQARVL EAILKHGDVE EAVRIVKEVT
KOD          598   DEEGKITTRG LEIVRRDWSE IAKETQARVL EALLKDGDVE KAVRIVKEVT
Vent         601   DEEGRITTRG LEVVRRDWSE IAKETQAKVL EAILKEGSVE KAVEVVRDVV
Deep         599   DEEGKIITRG LEIVRRDWSE IAKETQAKVL EAILKHGNVE EAVKIVKEVT
JDF-3        598   DEEGKITTRG LEIVRRDWSE IAKETQARVL EAILRHGDVE EAVRIVREVT

Pfu          649   QKLANYEIPP EKLAIYEQIT RPLHEYKAIG PHVAVAKKLA AKGVKIKPGM
Tgo          648   EKLSKYEVPP EKLVIYEQIT RDLKDYKATG PHVAVAKRLA ARGIKIRPGT
KOD          648   EKLSKYEVPP EKLVIHEQIT RDLKDYKATG PHVAVAKRLA ARGVKIRPGT
Vent         651   EKIAKYRVPL EKLVIHEQIT RDLKDYKAIG PHVAIAKRLA ARGIKVKPGT
Deep         649   EKLSKYEIPP EKLVIYEQIT RPLHEYKAIG PHVAVAKRLA ARGVKVRPGM
JDF-3        648   EKLSKYEVPP EKLVIHEQIT RELKDYKATG PHVAIAKRLA ARGVKIRPGT

Pfu          699   VIGYIVLRGD GPISNRAILA EEYDPKKHKY DAEYYIENQV LPAVLRILEG
Tgo          698   VISYIVLKGS GRIGDRAIPF DEFDPAKHKY DAEYYIENQV LPAVERILRA
KOD          698   VISYIVLKGS GRIGDRAIPF DEFDPTKHKY DAEYYIENQV LPAVERILRA
Vent         701   IISYIVLKGS GKISDRVILL TEYDPRKHKY DPDYYIENQV LPAVLRILEA
Deep         699   VIGYIVLRGD GPISKRAILA EEFDLRKHKY DAEYYIENQV LPAVLRILEA
JDF-3        698   VISYIVLKGS GRIGDRAIPF DEFDPTKHKY DADYYIENQV LPAVERILRA

Pfu          749   FGYRKEDLRY QKTRQVGLTS WLNIKKs---
Tgo          748   FGYRKEDLRY QKTRQVGLGA WLKPKt----
KOD          748   FGYRKEDLRY QKTRQVGLSA WLKPKGt---
Vent         751   FGYRKEDLRY QSSKQTGLDA WLKr------
Deep         749   FGYRKEDLRW QKTKQTGLTA WLNIKKk---
JDF-3        748   FGYRKEDLRY QKTRQVGLGA WLKPKGkkk
```

Alignment (FASTA format):

```
>Pfu
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEE
VKKITGERHGKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKV
REHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGE
EFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIRE
KDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS--EPKMQRIGDMT
AVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKA
```

WESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSS
TGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLW
ENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPG
FIPSLLGHLLEERQKIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYY
GYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYAT
IPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVI
DEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVI
QKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPGM
VIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEG
FGYRKEDLRYQKTRQVGLTSWLNIKKs—

>Tgo
MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIED
VKKITAERHGTTVRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKI
KEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGE
EFAEGPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKE
KDPDVLITYNGDNFDFAYLKKRSEKLGVKFILGREGS—EPKIQRMGDRF
AVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQA
WETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDERELARR-RESYAGGYVKEPERGLW
ENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPG
FIPSLLGDLLEERQKVKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYY
GYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFAT
IPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVI
DEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVT
EKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRA
FGYRKEDLRYQKTRQVGLGAWLKPKt—

>KOD
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEE
VKKITAERHGTVVTVKRVEKVQKKFLGRPVEVWKLYFTHPQDVPAIRDKI
REHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGE
EFAEGPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKE
KDPDVLITYNGDNFDFAYLKKRCEKLGINFALGRDGS—EPKIQRMGDRF
AVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPA
WETGENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDEKELARR-RQSYEGGYVKEPERGLW
ENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPG
FIPSLLGDLLEERQKIKKKMKATIDPIERKLLDYRQRAIKILANSYYGYY
GYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYSDTDGFFAT
IPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVI
DEEGKITTRGLEIVRRDWSEIAKETQARVLEALLKDGDVEKAVRIVKEVT
EKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRA
FGYRKEDLRYQKTRQVGLSAWLKPKGt—

>Vent
MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEE
IKAIKGERHGKTVRVLDAVKVRKKFLGREVEVWKLIFEHPQDVPAMRGKI
REHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGD
EFGKGEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFvQVVKE
KDPDVIITYNGDNFDLPYLIKRAEKLGVRLVLGRDkehpEPKIQRMGDSF
AVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAI
WETEESMKKLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSS
TGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRTTYLGGYVKEPEKGLW
ENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPG
FIPSILGDLIAMRQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYM
GYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKVLYADTDGFYAT

IPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVI
DEEGRITTRGLEVVRRDWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVV
EKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARGIKVKPGT
IISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEA
FGYRKEDLRYQSSKQTGLDAWLKr———

>Deep
MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDE
VRKITAERHGKIVRIIDAEKVRKKFLGRPIEVWRLYFEHPQDVPAIRDKI
REHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGE
EFAKGPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIRE
KDPDVIITYNGDSFDLPYLVKRAEKLGIKLPLGRDGS—EPKMQRLGDMT
AVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEA
WETGKGLERVAKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSS
TGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESYAGGYVKEPEKGLW
EGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPG
FIPSLLKRLLDERQEIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYY
GYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLYIDTDGLYAT
IPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALI
DEEGKIITRGLEIVRRDWSEIAKETQAKVLEAILKHGNVEEAVKIVKEVT
EKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVKVRPGM
VIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEA
FGYRKEDLRWQKTKQTGLTAWLNIKKk—

>JDF-3
MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEE
IKKITAERHGRVVKVKRAEKVKKKFLGRSVEVWVLYFTHPQDVPAIRDKI
RKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGE
EFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKE
KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGS—EPKIQRMGDRF
AVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATA
WETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDERELARR-RggYAGGYVKEPERGLW
DNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPG
FIPSLLGNLLEERQKIKRKMKATLDPLEKNLLDYRQRAIKILANSYYGYY
GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHAT
IPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVI
DEEGKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVT
EKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRA
FGYRKEDLRYQKTRQVGLGAWLKPKGkkk

Sequence tree:
==========

Tree constructed using UPGMA

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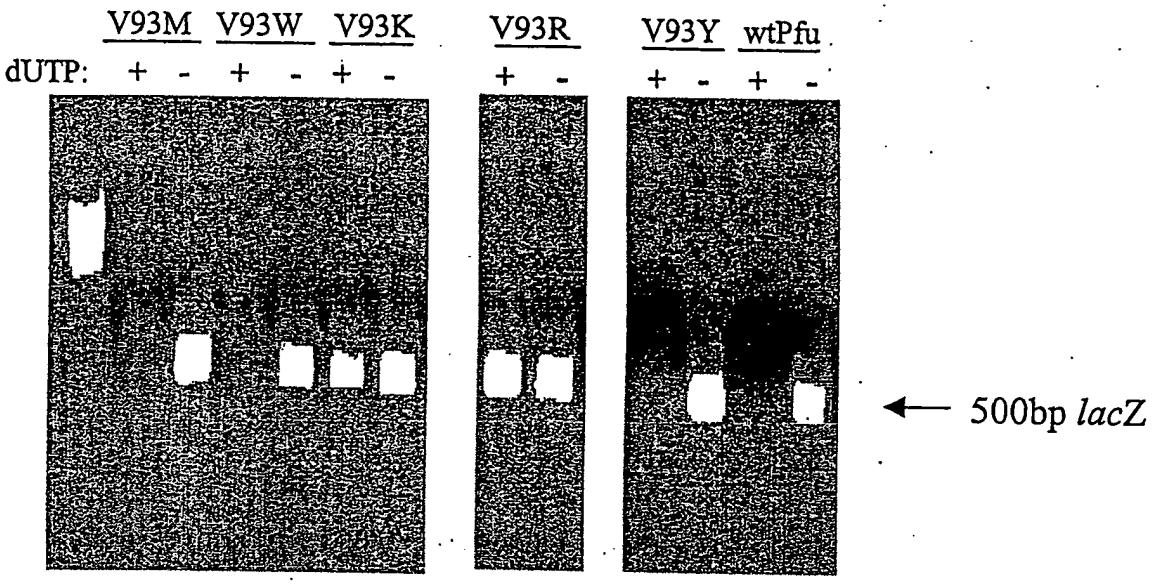
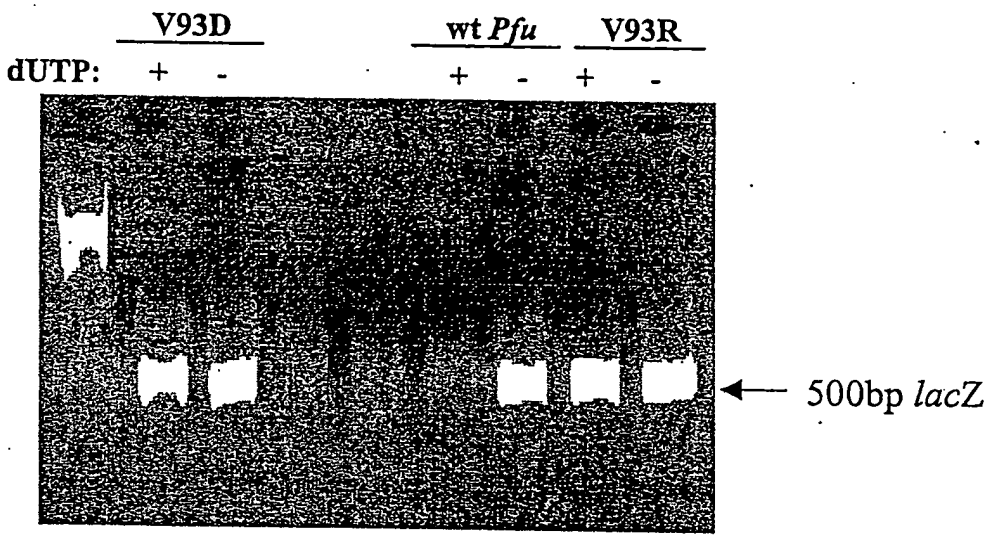
Deep :0.000998):0.000080,
((Tgo :0.000905,
KOD :0.000905):0.000032,
JDF-3 :0.000937):0.000141):0.000067,
Vent :0.001144);



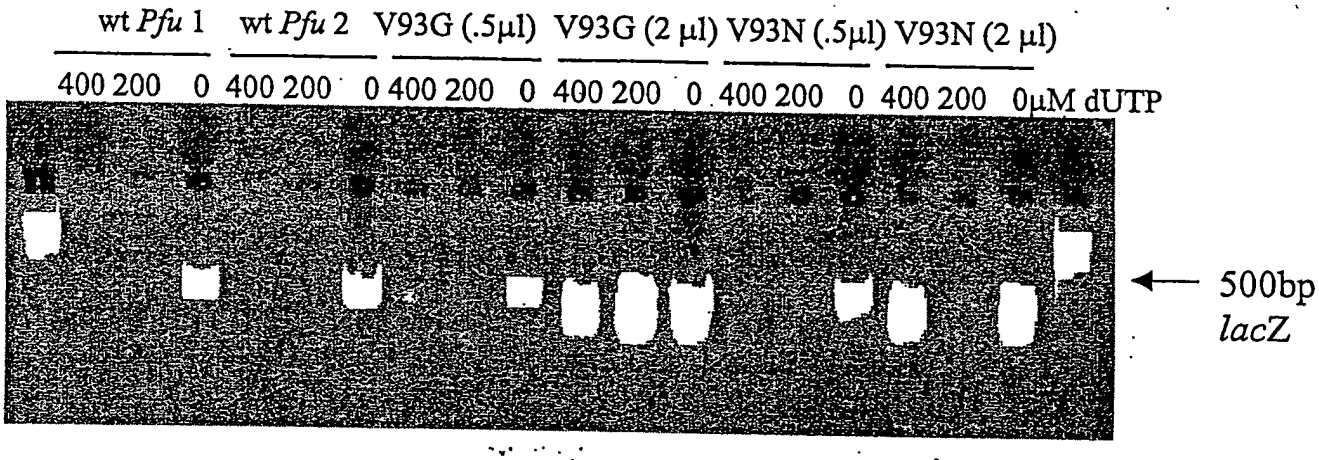
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

Figure 8A



Results: The *Pfu* V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*.

Figure 8B



Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 8C

Figure 9: Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65°

Figure 10. **Oligonucleotide Primers for QuikChange Mutagenesis**

KOD V93 mutations

V93Q KOD 5′- CTCATCCG CAGGACCAGC CAGCGATAAG GGACAAG-3′ (SEQ ID NO: 56)

V93R KOD 5′- CTCATCCG CAGGACCGTC CAGCGATAAG GGACAAG-3′ (SEQ ID NO: 57)

V93K KOD 5′- CTCATCCG CAGGACAAAC CAGCGATAAG GGACAAG-3′ (SEQ ID NO: 58)

V93N KOD 5′- CTCATCCG CAGGACAATC CAGCGATAAG GGACAAG-3′ (SEQ ID NO: 59)

V93E KOD 5′- CTCATCCG CAGGACGAGC CAGCGATAAG GGACAAG-3′ (SEQ ID NO: 60)

V93D KOD 5′- CTCATCCG CAGGACGATC CAGCGATAAG GGACAAG-3′ (SEQ ID NO: 61)

Tgo V93 mutations

(SEQ ID NO: 62)

V93Q Tgo 5′-CAC CCC CAG GAC **CAA** CCC GCA ATC AGG GAC AAG G-3′

(SEQ ID NO: 63)

V93R Tgo 5′-CAC CCC CAG GAC **AGA** CCC GCA ATC AGG GAC AAG G-3′

(SEQ ID NO: 64)

V93N Tgo 5′-CAC CCC CAG GAC **AAT** CCC GCA ATC AGG GAC AAG G-3′

(SEQ ID NO: 65)

V93K Tgo 5′-CAC CCC CAG GAC **AAA** CCC GCA ATC AGG GAC AAG G-3′

(SEQ ID NO: 66)

V93E Tgo 5′-CAC CCC CAG GAC **GAA** CCC GCA ATC AGG GAC AAG G-3′

(SEQ ID NO: 67)

V93D Tgo 5′-CAC CCC CAG GAC **GAC** CCC GCA ATC AGG GAC AAG G-3′

JDF-3 V93 mutations

(SEQ ID NO: 68)

V93Q JDF-3 5′-ACG CAC CCG CAG GAC CAA CCG GCA ATC CGC GAC 3′

(SEQ ID NO: 69)

V93R JDF-3 5′-ACG CAC CCG CAG GAC CGT CCG GCA ATC CGC GAC 3′

(SEQ ID NO: 70)

V93E JDF-3 5′-ACG CAC CCG CAG GAC GAG CCG GCA ATC CGC GAC 3′

(SEQ ID NO: 71)

V93D JDF-3 5′-ACG CAC CCG CAG GAC GAT CCG GCA ATC CGC GAC 3′

(SEQ ID NO: 72)

V93K JDF-3 5′-ACG CAC CCG CAG GAC AAA CCG GCA ATC CGC GAC 3′

***Pfu* deletions**

(SEQ ID NO: 73)

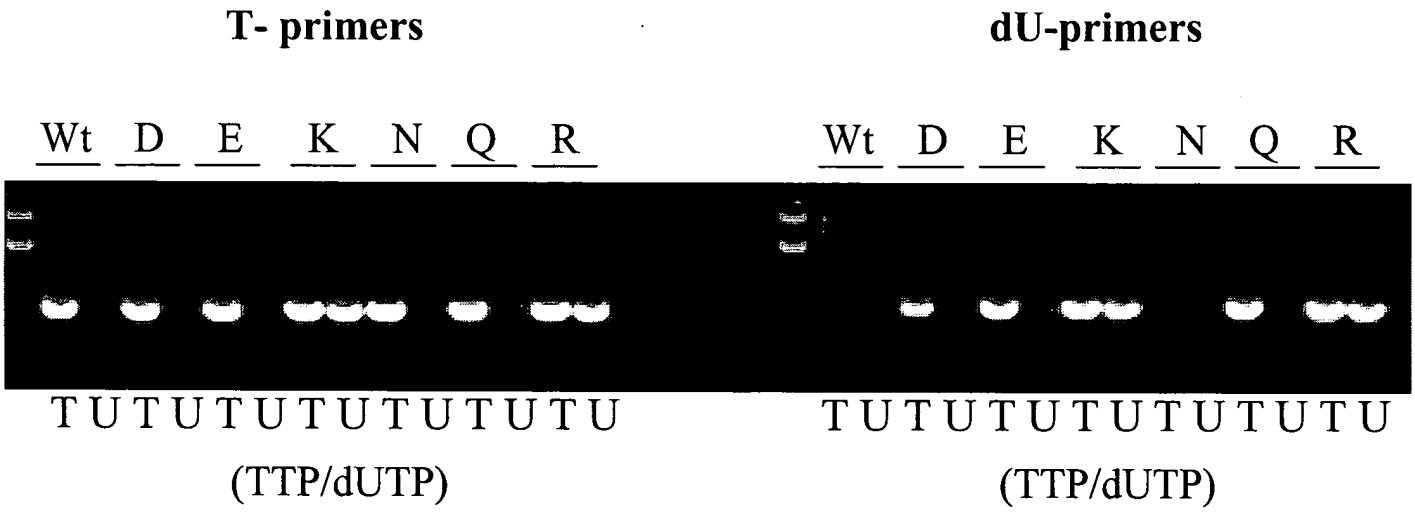
Δ93 Pfu : 5′- GAA CAT CCC CAA GAT CCC ACT ATT AGA G-3′

(SEQ ID NO: 74)

Δ92-94 Pfu : 5′- GAA CAT CCC CAA ACT ATT AGA G-3′

Fig. 11. Uracil Insensitivity of KOD V93 mutants

T-/dU-primers and dUTP/TTP incorporation:



	With regular primers		With U primers	
	dNTP	dGCAU	dNTP	dGCAU
KOD WT	+	-	-	-
KOD V93D	+	-	+	-
KOD V93E	+	-	+	-
KOD V93K	+	+	+	+
KOD V93N	+	-	-	-
KOD V93Q	+	-	+	-
KOD V93R	+	+	+	+

Fig. 12. Uracil Insensitivity of Tgo V93 mutants

T-primers and dUTP/TTP incorporation:

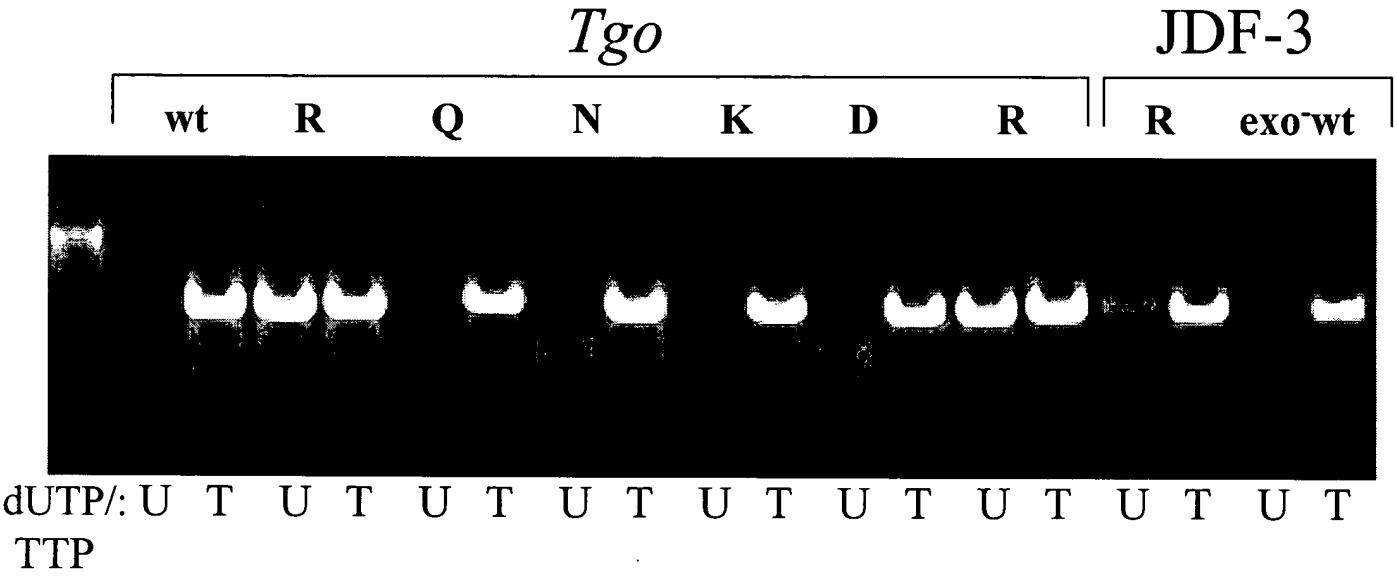
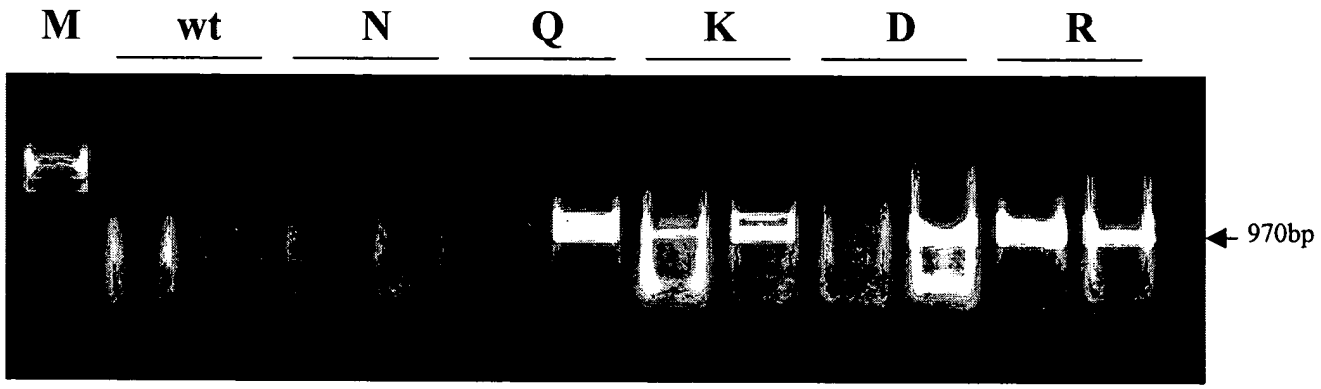


Fig. 13. Uracil Insensitivity of JDF-3 V93 mutants

T-primers and dUTP/TTP incorporation:



T-/dU-primers and dUTP/TTP incorporation:

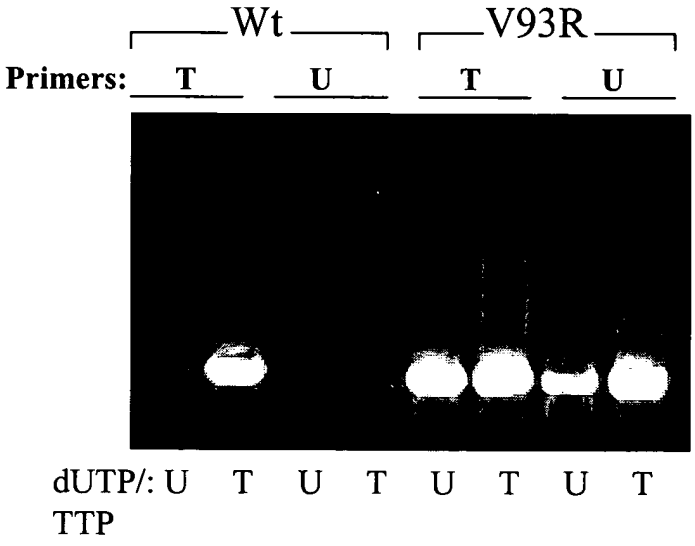
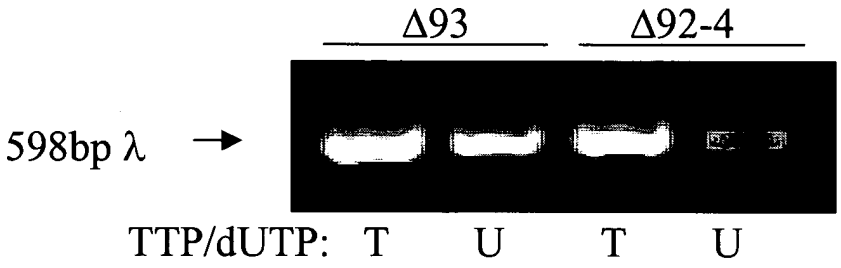
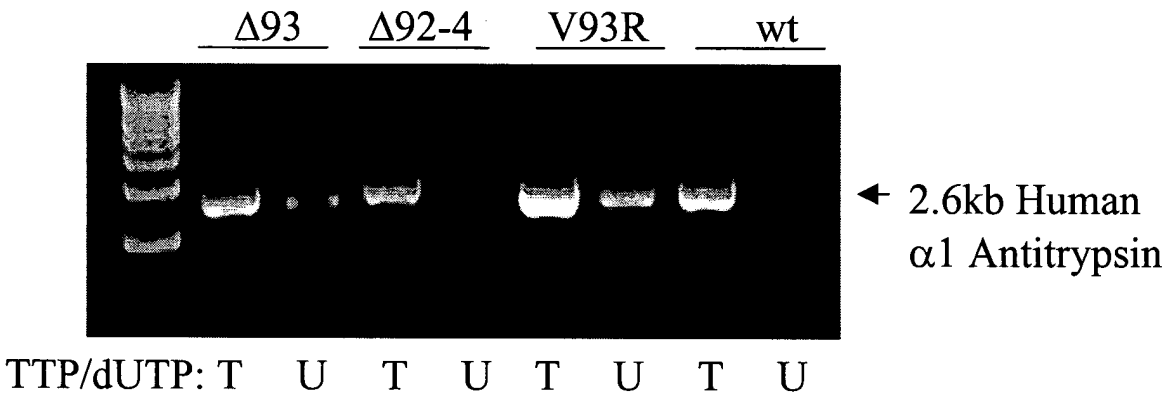


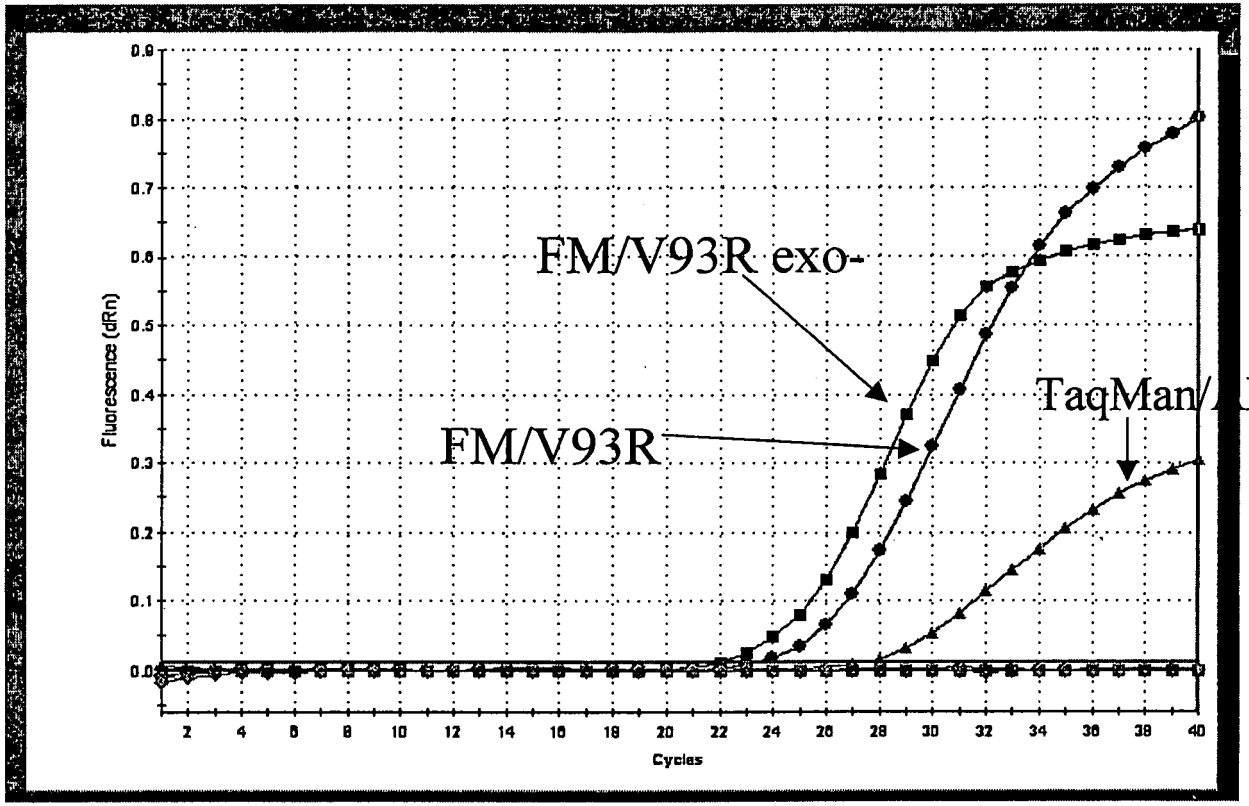
Fig. 14. Uracil Sensitivity of *Pfu* deletion mutants

T-primers and dUTP/TTP incorporation:





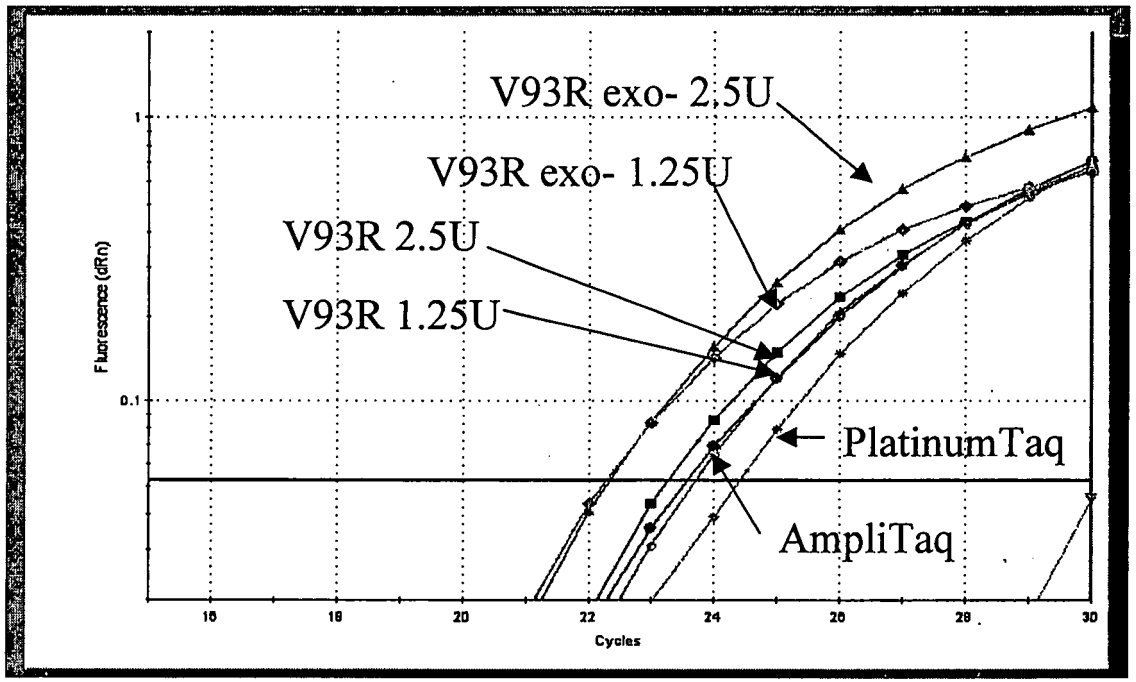
Amplification Plot for Comparison of Three Polymerases in QRT-PCR



* FM = FEN-1

Figure 15

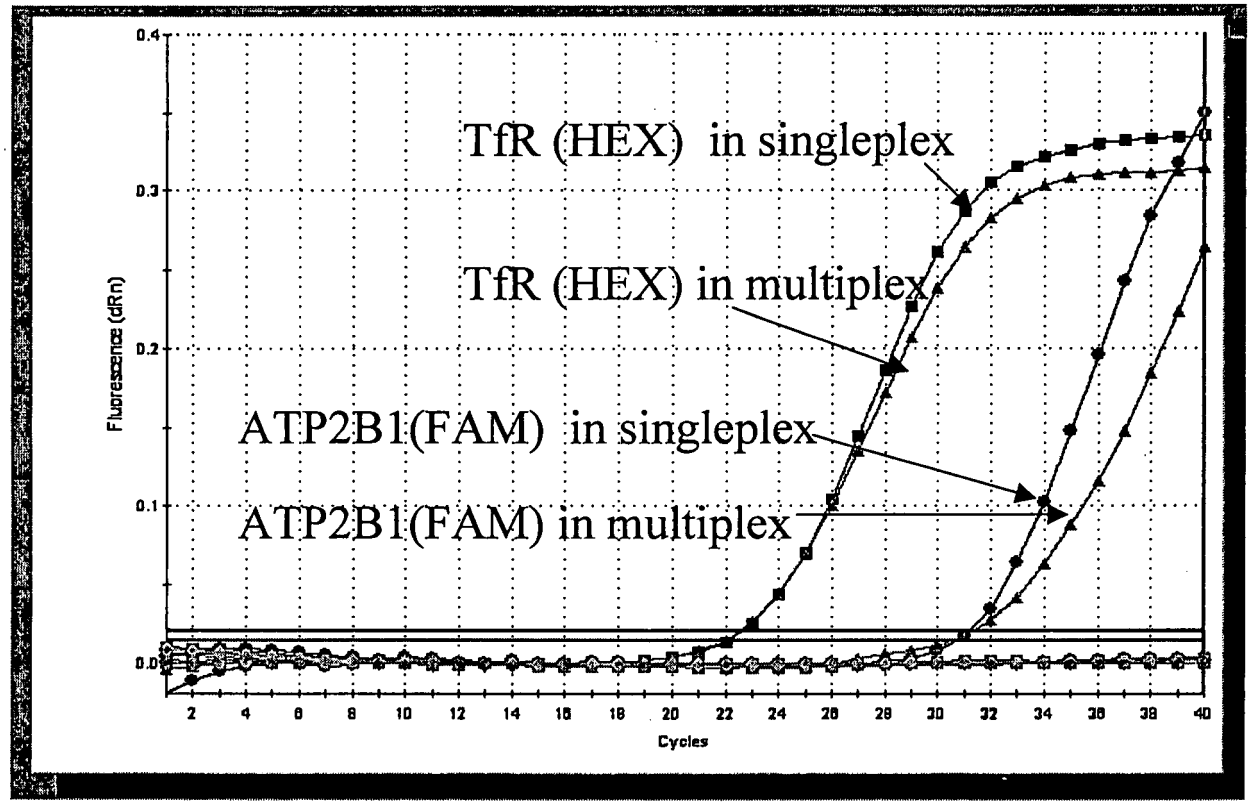
Semi-log Amplification Plots Comparing Pfu V93R and Pfu V93R exo- Containing QPCR Reactions



	V93R exo-	V93Rexo-	V93R	V93R	PlatinumTaq	AmpliTaq
Units	1.25	2.5	1.25	2.5	1.25	1.25
Avg Ct	22.2	22.2	23.5	23.2	24.3	23.6

Figure 16

Pfn V93R exo ***-Multiplex-ATP2B1 and TfR***



	Target amt	TfR	ATP2B1	TfR + ATP2B1
Pfn V93R exo	100ng	**22.8**		**22.7**
			30.9	30.8
ABI MM	100ng	**24.6**		**25.3**
(TaqMan)			30.3	30.1

Figure 17